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	LOCUS	CNS0091P	925 bp	DNA	linear	GSS 03-JUN-1999
	DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19016 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
	ACCESSION	AL053013				
	VERSION	AL053013.1 GI:4934461				
	KEYWORDS	GSS.				
	SOURCE	Drosophila melanogaster (fruit fly)				
	ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 925)				
	REFERENCE	Direct Submission				
	AUTHORS	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segreif@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
	JOURNAL	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.				
	FEATURES	Location/Qualifiers				
	Source	1..925				
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		/mol_type="genomic DNA"				
		/db_xref="taxon:7227"				
		/clone="BACR19016"				
		/clone_lib="RPCT-98"				
		/note="end : TET3"				
	BASE COUNT	120 a 61 c 61 g 172 t 511 others				
	ORIGIN					
	Query Match	0.6%; Score 41.4; DB 29; Length 925;				
	Best Local Similarity	13.0%; Pred. No. 87;				
	Matches	46; Conservative 154; Mismatches 153; Indels 0; Gaps 0;				
Oy	5826	TTTTCGGCCGTAAAGCGCTGACCACCAAGCGCGGCAGCAGCACCGATCTTTATGCGCGCTT	5885			
Db	550	TTTTTSSSGTGKGGSSGSGBSCGCCSSCSGCCBCCCCSCSYCCSSBSBSX	609			
Oy	5886	GCCAACGACAGAGAGCGAGCCCTTAGTGTCAGAAATCGTTCCGGGGCGAAGCTGA	5945			
Oy	610	CSSTSBSCSCCCSSSKSVCTGSCSSSSSCSSSSSTSSSTSSSTSSKSSSSSSSSS	669			
Db	5946	AAGTAACGGCGCGCTTGCTGTACTAATGAATCAGATGCGTCCCATGAATATG	6005			
Oy	670	TTSKTSASGSGSWAGGSGSGTSSSSSSSTSSSVSSSGSKSTBSGBSSG	729			
Oy	6006	AGATTTCCTACACAGTGCAGCGACAACGACTGTACCCGCGCGCGAGATCGTATC	6065			
Db	730	SSSSSSSTSBSCTSTSSSSSSSSYSTSCCTCCCSYSTSSSSSTSMGSTRSSSS	789			
Oy	6066	GCGAAGCGGCGCCGTGTCATCAACCGTCATTTCCCTTCGCGCATGGAAGCTTG	6125			
Db	790	SSVGTSSSSSDSTSTCCSCCYWCTCCTBYMBCTSTCGGSSSSGKGVTWKCGCGCG	849			
Oy	6126	GCTTCGCTGAAGCTCTTCCTGCTTCGGCACCCGTTTGATGATGAGCGCGCGG	6178			
Db	850	SSSTNGMGTSACSSSSSSCGSSSSSSSKSSASSSSVSSGSSGVASNSSS	902			

RESULT 12	CD433849/c	869 bp	mRNA	linear	EST 03-JUN-2003
LOCUS	CD433849				
DEFINITION	EU010315H03.b Endosperm_3 Zea mays cDNA, mRNA sequence.				
ACCESSION	CD433849				
VERSION	CD433849.1	GI:31349492			
KEYWORDS	EST.				
ORGANISM	Zea mays				
SOURCE	Zea mays				
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 869) Lai, J., Dey, N., Kim, C. S., Becraft, P., Larkins, B., Linton, E. and Messing, J.				
TITLE	Sequencing of the maize endosperm ESTs				
JOURNAL	Unpublished				
COMMENT	Contact: Lai, Jinseng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 190 Freilichpuyen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-5735 Email: jlai@waksman.rutgers.edu. Seq primer: T3.				
FEATURES	Location/Qualifiers				
SOURCE	1..869 /organism="Zea mays" /mol_type="mRNA" /cultivar="W2" /db_xref="taxon:4577" /cruise_type="Endosperm of 7-23DAP" /clone_lib="Endosperm 3" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"				
BASE COUNT	104 a 301 c 316 g 148 t				
ORIGIN					
Query Match	0.6%; Score 41; DB 14; Length 869;				
Best Local Similarity	52.0%; Pred. No. 1.1e+02;				
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;					
Qy	6501 ATGACGACATTGGCGAGAGGATGGATTAGAGCTCTGTGACATGAGAGCGCATCAAGTTC	6560			
Db	569 ATGACGGCCTTCGACGACGACGCGCGTGCAGTCCCGGACCCCGGACGCGAGCGGACACCC	510			
Qy	6561 GCGCTGCTGTGACAGCGCTATGCTGTCTGTCTGGAAAGCAAGCGCGGCTTTGTGCACAAAGC	6620			
Db	509 GCGCGGCGCATGCCCCCGGCGGAGAGCCGAGAGAGCGCTGGGCGAGCGGCGCCAGC	450			
Qy	6621 TAATCAGCTTGGCAGTTCACGATGCGGCGCGAGCGAGGAAAGAGCGGCTGTCAAGC	6677			
Db	449 AGCTGCCGACCCAGTGAAGACCGCGCGACCTAAGGAGAGCGCGCCGCCGACGAGC	393			
RESULT 13	AM776190/c	375 bp	mRNA	linear	EST 07-SEP-2000
LOCUS	AM776190				
DEFINITION	EST333255 DBTL Medicago truncatula cDNA clone pBSIL-6H15, mRNA sequence.				
ACCESSION	AM776190				
VERSION	AM776190.1	GI:7766003			
KEYWORDS	EST.				
SOURCE	Medicago truncatula (barrel medic)				
ORGANISM	Medicago truncatula				
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.				
AUTHORS	1 (bases 1 to 375) Fedotova, M., Pierson, B. L., Samac, D. A., Vance, C. P., Gantt, G. S., Peng , H., Ellis, L., Town, C. D., Bowman, C. L., Craven, M. B., Hansen, T. S.,				

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JOURNAL
COMMENT

Unpublished
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene T3 primer.

FEATURES

source

1..535
Location/Qualifiers

/organism="Triticum monococcum"
/mol_type="mRNA"
/cultivar="DV92"
/db_xref="taxon:4568"
/clone="WHE0598_D04_H08"
/tissue_type="Vegetative shoot apex"
/dev_stage="Three weeks-old plants"
/lab_host="E. coli XL0LR"
/clone_lib="Triticum monococcum vegetative apex cDNA
library"
/note="Vector: Lambda pBK-CMV (Lambda Zap Express),
excised phagemid; Site_1: EcoRI; Site_2: XhoI; The tissue,
total RNA, and poly(A) RNA were prepared, a cDNA library
was made, and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
, J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the Olin Anderson Lab (all
other authors)."

BASE COUNT 119 a 144 c 146 g 126 t
ORIGIN

Query Match

Best Local Similarity 50.5%; Score 40.4; DB 10; Length 535;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

OY	6712	TGCTGGCGCACTAGAGTGCCTCTGATGCTCCATCATCGGCAGCAACTGGAAGCAGC	6771
DB	15	TGGTTGATAGAGATCTGCACCGACGACGCGGGGAGAAAGCAGAGTTAC	74
OY	6772	GCTGGCATAGTAGGCGACCGCGCATTAAGTCGTGGAGCAAGCTGGAGCTGGGGTT	6831
DB	75	AGGGGACAGCCGCGGCAAGAGATCAGACAGATCGATGCGGAGCTGCGGGAGCGACG	134
OY	6832	GCGAGGTTAAGTTACGACAGAGGGGAGACATATGGAAGCTTCGTTACAGCCGTTG	6891
DB	135	GCGTGTGAAGACCTCGTCTCGCGCGTTCAAGAGAGGAGCGCGGAGGCGCTCG	194
OY	6892	TCCGCTTATCCAC	6905
DB	195	ACCAGCTATCCGC	208

Search completed: January 31, 2004, 13:57:56
Job time : 884.7secs

[illegible][illegible]

LOCUS	CNS015XR	1159 bp	DNA	linear	GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BACN15017 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL106041				
VERSION	AL106041.1 GI:5619746				
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peiryoza; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1159)				
REFERENCE	Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : fr BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.				
FEATURES	Location/Qualifiers				
source	1..1159 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACN15017" /clone_1fb="DrosBAC" /plasmid="pBelobAC11" /note="end : T7"				
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ORIGIN					
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Best Local Similarity	17.6%; Pred. No. 48; Mismatches 144; Indels 3; Gaps 1;				
Matches	67; Conservative 167; Mismatches 144; Indels 3; Gaps 1;				
QY	3617 TGTCTTCACATCGCGAAGCTTGATCTGTCGGAATCGGAGCGGCTTTCGCGTCTT 3676				
DB	781 TSTBTBSTDYTKTSBYYTBTBMSWTTTATATASCSTBSBSSSTBSBTCKSTSTS 840				
QY	3677 TATCAACATGCTCGAATGGGTTTCTTGCACTTACTGAGTGGTGGTGATGAGCAAACTT 3736				
DB	841 TSSBABATWSVTYTKTSTSTSBCTBYTBYSKSTBSBBSBTBSBBBSBTBCKSTSTK 900				
QY	3737 TCCGGAATCGCGGTTTATTTATCCCGTTTTCCTTGATGGAATGACAGCGCACT 3796				
DB	901 SBSTSTSBSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 957				
QY	3797 TGCAGTGGCGCTTGAGCGCTGACGGAAGTTGATTAAGCCGCGCCGCTTCCCG 3856				
DB	958 TSTTCKSKGTSSTSSBSSSSSBSTSSSSBBSBKBTBTGTSSTBSSTSTSTSSBB 1017				
QY	3857 GCTGACGCTCTTGATCGCGCGTTTACAGACGATTCGTGCTGCTCTTGATCTACGT 3916				
DB	1018 TSSBSBSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSS 1077				
QY	3917 TGAATTAAGCTGTGACCAATCGGAGCAATTTGCTCTCCGCTGTCGTCGCGAAT 3976				
DB	1078 TBBBSBSBTBSBTTSTSTSTSTSBCTTTTSSSSSTSSSSSSSTSTSTSSBSBTT 1137				
QY	3977 GGGCGTACTTTTCCGATCTG 3997				
DB	1138 SBATTBSTSTBTBTTBSTSTS 1158				

[illegible]

Accession	Version	KeyWords	Source	Organism	Reference	Authors	Title	Journal	Comment
clone CSODI079YN16	3-PRIME, mRNA sequence.								
BR361080	GI:30374504								
EST.									
Homo sapiens (human)									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1 (bases 1 to 1201)									
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.									
Full-length cDNA libraries and normalization									
unpublished									
Contact: Genoscope									
Genoscope - Centre National de Sequencage									
BP 191 91006 Evry cedex - France									
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr									
Library was constructed by Life Technologies, a division of									
Invitrogen. Contact : Feng Liang Email : fliang@life tech.com URL :									
http://fulllength.invitrogen.com/Invitrogen Corporation 1600									
Paradey Avenue Genoscope sequence ID : CSODI079D508NPl.									
Location/Qualifiers									
1..1201									
/organism="Homo sapiens"									
/mol_type="mRNA"									
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/clone="CSODI079YN16"									
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/note="1st strand cDNA was primed with a NotI-oligo (dN) primer. Five prime end enriched, double-strand cDNA was									
digested with Not I and cloned into the Not I and EcoR V									
sites of the pCMVSPORT 6 vector. Library was normalized."									
BASE COUNT	155 a 152 c 130 g 182 t 582 others								
ORIGIN									
Query Match	0.6%; Score 44.8; DB 13; Length 1201;								
Best Local Similarity	8.9%; Pred. No. 14;								
Matches 35; Conservative 198; Mismatches 160; Indels 1; Gaps 1;									
OY	3605 GGATTGGAAGATGCTTCCTCACTCGGAAGCTTGATGTCGGAATCGGGACGGCT								
DB	805 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK								
OY	3665 TTTCGCGCTTTTATCAACATGCTCGAATGGGGTTCCTGATTAGTTGGGTGGT								
DB	865 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK								
OY	3725 GCGACGAAAGTTCCGCAATCGCGGTTTTTATTTCCCGTTTTCACTTTGGTGAAT								
DB	925 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK								
OY	3785 GAGCAGCGGAGCTTGCGATTTGGGCTTGAGCGCTCACTCACCGAAGCTTGATTAGCGCGG								
DB	984 TTTTATTTTTHNNKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK								
OY	3845 CCGGTTTCCCGGCGTGCAGCTTTCATGCGCGCTTATACAGCATTTGCTGCTGCTT								
DB	1044 KHMNNNNNNKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK								
OY	3905 CTGATCTACGTTGGATTAAATAGGTGTAGACATCGAATATTTGCTTCGCGCTGC								
DB	1104 CCKKCCCBCCCKKCCBCCGCCCKKKKKKCKKKKKKCCCKKKKKKCCCKKKKKCC								
OY	3965 GCTTCCCGGATTTGGCGCTACTTTTCTGATCTGC 3998								
DB	1164 CCKBCKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK								
RESULT 6									
LOCUS	CNS0079HK	948 bp	DNA	linear	SSS 03-JUN-1999				
DEFINITION	BAC15103 of RPlC-98 library from Drosophila melanogaster (fruit								

ACCESSION	FLY), genomic survey sequence.
AL067579	
AL067579.1	GI:4945739
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryotes: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS	1 (bases 1 to 948)
TITLE	Genoscope.
JOURNAL	Direct Submission
COMMENT	Submitted (02-JUN-1999) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
FEATURES	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Osoegawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 18ogenic strain Y2; cm bw sp. the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .
SOURCE	Location/Qualifiers
	1..948
	/organism="Drosophila melanogaster"
	/mol_type="genomic DNA"
	/db_xref="taxon:7227"
	/clone="BACR15103"
	/clone_lib="RPCT-98"
	/note="end : TET3"
BASE COUNT	265 a 74 c 134 g 187 t 288 others
ORIGIN	
Query Match	0.6%; Score 43; DB 29; Length 948;
Best Local Similarity	25.7%; Pred. No. 36;
Matches 101; Conservative 105; Mismatches 187; Indels 0; Gaps 0;	
QY	6021 GTGGCGGACGACACTGTCTACGGGGCGGCGGAGTCTGTATCGGAGCGGCCCGT 6080
DB	556 BTGCGKTKSSGATGTVARGGGGRKSMVDRBGTGCTCGCBRTATYTGSTISGTGCTSKG 615
QY	6081 GGTGATCAACCGTATTTCCTCTCTCGGCGCATCTGGAAGCCTCTGAGCTTCCTGAACTC 6140
DB	616 TWCTGTATTTTNTTSTTTTGGGTGTRKSGGGGGGSGTGKGGGSGKSGKSGKSGKSGTGG 675
QY	6141 CTTCCGTTGTGCGACCGGTTTCATGAGCGCGCGCGGAGACATTTATCGTTTTCAGAG 6200
DB	676 TSKCGKSGSKGASBKGKTKGGGGGATGTSKSKGSGSCTTTTGGTTTGGTGGBSG 735
QY	6201 GTGAGTTTGTCAACCGAGCCCTTGTGTGCGAGAGGAGGCTTTCCGCAATTGGAATGATGT 6260
DB	736 TYSTSCTSTTCTCCGGGSSGTSKSGSGGCGGGAATGKRTGTATTTGRRVTTTC 795
QY	6261 TGGCGGACGACGAGTCCACCGCTCTGTTCAACCTCCGGAATCTCGATGTGCGCG 6320
DB	796 AGAASKACATVAVBTITGYCCBTSSSCTCTSSSTTBSBSGCGTTCTSATSSGCG 855
QY	6321 ATTGCTTGGGCGTAACTCGGTAGAGGTCAACGTAATGACACTCGACACAGGCC 6380
DB	856 TTTTSTTSGTGGCTCTSGCTCTCGTBTBTTCGCGWCCGMCNCKGTISGVRCTGTS 915
QY	6381 CATGAACATGTTTGGCGGTCAAGATTCCTG 6413
DB	916 STBSGCVKKGCTGCTTYSGSGKSBSCCG 948

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 05:43:15 ; Search time 8837 Seconds
(without alignments)
19642.703 Million cell updates/sec

Title: US-09-927-616A-1
Perfect score: 7142
Sequence: 1 CGCGTAAAGACAGCAGCAG.....ACATCAGATCGCAGACGCG 7142

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 segs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estnu:*
4: em_estnu:*
5: em_estnu:*
6: em_estnu:*
7: em_estnu:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estfun:*
17: em_gss_hum:*
18: em_gss_hum:*
19: em_gss_hum:*
20: em_gss_vit:*
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24: em_gss_vit:*
25: em_gss_vit:*
26: em_gss_vit:*
27: em_gss_vit:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	53.8	0.8	910 29	CNS0060N
2	50	0.7	1201 13	BX381961
3	46.4	0.6	1201 13	BX381961
4	45.6	0.6	1201 13	BX356664

Result No.	Score	Query Match Length	ID	Description
5	44.8	0.6	1201 13	BX361080
6	43	0.6	948 29	CNS007HK
7	42.6	0.6	1159 29	CNS015XR
8	42.4	0.6	885 23	BX425603
9	42.4	0.6	902 29	CNS0060P
10	41.6	0.6	712 13	BX416727
11	41.4	0.6	925 29	CNS0091P
12	41	0.6	869 14	CD433849
13	40.6	0.6	375 9	AW776190
14	40.6	0.6	992 10	BF577523
15	40.4	0.6	535 10	BF199915
16	40.4	0.6	552 12	BMS51928
17	40.4	0.6	765 29	BX226817
18	40.4	0.6	864 12	B1668178
19	40.4	0.6	1044 29	CNS00K3G
20	40.2	0.6	1201 9	AL514118
21	40.2	0.6	1201 13	BX446296
22	40	0.6	1201 13	BX360624
23	40	0.6	1201 13	BX400034
24	39.8	0.6	510 13	BQ748115
25	39.8	0.6	937 29	CNS006XP
26	39.8	0.6	1434 12	BG855023
27	39.6	0.6	487 12	BT721733
28	39.6	0.6	521 13	BX109274
29	39.6	0.6	736 13	B0653659
30	39.6	0.6	822 13	B0954877
31	39.6	0.6	856 29	B2676846
32	39.4	0.6	646 12	BM185162
33	39.4	0.6	769 29	CNS016UY
34	39.4	0.6	1201 13	BX361152
35	39.2	0.5	701 12	BM652341
36	39.2	0.5	954 12	B1694420
37	39.2	0.5	1101 29	CNS001YH
38	39	0.5	397 9	AW13801
39	39	0.5	669 13	BX465136
40	39	0.5	683 29	B7728315
41	39	0.5	723 10	BB651318
42	39	0.5	781 11	AK006747
43	39	0.5	791 28	BH565091
44	39	0.5	807 29	CNS0119V
45	39	0.5	912 29	CNS029BV

ALIGNMENTS

RESULT 1
CNS0060N 910 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL065629.1 GI:4944698
VERSION 1
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 910)
AUTHORS Genoscope.
TITLES Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oosagawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of


```

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C248
; CURRENT APPLICATION NUMBER: US/10/142, 885
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-885-10

Query Match      0.6%; Score 40.4; DB 13; Length 594;
Best Local Similarity 8.1%; Pred. No. 0.24;
Matches 44; Conservative 194; Mismatches 303; Indels 1; Gaps 1;

QY 4368 GGAGAGATCCGCTTGCATCCAGACGCTTCAATCCGGAGTGAAGCGGTTGCAAG 4427
DB 21 KRAERRREYERKIKDPAQFLQVHGRACKVHLSAVALAESPVMMPWQDNTNMIDRF 80
QY 4428 GCGTCATGCTCGAAGTACCAATGCTTCAACAGAGATCCGTCACCTCGCTGAG 4487
DB 81 DVRAHLDHLPDYTPPLTTTISPESDERKCYERYGLVNDPAGISEBCLYIYIDE 140
QY 4488 CTGTGCTGAACGGCGCCATCTGTGCTGATCGCGGCAACAATCTCAAGATTGC 4547
DB 141 LVGLQRPSEDEKKTLEKKAISGYTEDSTVAEVEKAEKEEESAEESNSDEDEV 200
QY 4548 CGCAATCCCGCGGCAAGGAGATGACAGCGGCTCAATAGATTAGAGCGCGG 4607
DB 201 IPDIDVEVDVDELNOEVDALNKQATYGMADGDFVRLRKDEBAIKHAKLEBEKA 260
QY 4608 CTGAACGCTCGTTGACAGATGACAGATCTCTTCTTAAGTTGGCCAGATCCGAG 4667
DB 261 MYSGRRSRQRERFERKRLRGKISPPSYARSDPTDYPKRSPESSSRSRSPPTP 320
QY 4668 AGACGGTTCAACAGCTTGGTACAGATCGAGGCTCCGCGGATTTCTACTGCTTGC 4727
DB 321 GREKTFITSPGSDDEPMAAAMAAASGVTTGKPPAPQPGGAPAGRNASARRSSSS 380
QY 4728 CAACGCCGCTTGGCGGACATGTCGTTGGGTTCCGCACT-TCGCAAGAACGAGAG 4786
DB 381 SSSSSASRTSSRSRSGGYYRSGRHARSRSWSRSRSPSSSRSPSSSRGR 440
QY 4787 CGGAGTGAAGCTGCACTAGTGAAGCCATGAGTGAAGTGGTGGGGAGGATTAAG 4846
DB 441 RHSGGSRDGHYRSRPARGGYGRRRSRSHSGDYYRRGRLRHSSSRSSWSL 500
QY 4847 GTCCGGCGGAGACGCGGCTGTGAGAGTTCCCTCGCAACAGCAAAATCGGTTTGC 4906
DB 501 SPSSRSRLTRSHSPSPSGRSRSRSPSPSPAREKLTLPAAAPVGEKLTKEPBA 560
QY 4907 AG 4908
DB 561 AG 562

```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C448
; CURRENT APPLICATION NUMBER: US/10/158,790
; CURRENT FILING DATE: 2002-05-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-158-790-10

Query Match      0.6%; Score 40.4; DB 13; Length 594;
Best Local Similarity 8.1%; Pred. No. 0.24;
Matches 44; Conservative 194; Mismatches 303; Indels 1; Gaps 1;

QY 4368 GGAGAGATCCGCTTGCATCCAGACGCTTCAATCCGGAGTGAAGCGGTTGCAAG 4427
DB 21 KRAERRREYERKIKDPAQFLQVHGRACKVHLSAVALAESPVMMPWQDNTNMIDRF 80
QY 4428 GCGTCATGCTCGAAGTACCAATGCTTCAACAGAGATCCGTCACCTCGCTGAG 4487
DB 81 DVRAHLDHLPDYTPPLTTTISPESDERKCYERYGLVNDPAGISEBCLYIYIDE 140
QY 4488 CTGTGCTGAACGGCGCCATCTGTGCTGATCGCGGCAACAATCTCAAGATTGC 4547
DB 141 LVGLQRPSEDEKKTLEKKAISGYTEDSTVAEVEKAEKEEESAEESNSDEDEV 200
QY 4548 CGCAATCCCGCGGCAAGGAGATGACAGCGGCTCAATAGATTAGAGCGCGG 4607
DB 201 IPDIDVEVDVDELNOEVDALNKQATYGMADGDFVRLRKDEBAIKHAKLEBEKA 260
QY 4608 CTGAACGCTCGTTTGCAGATGACAGATCTCTTCTTAAGTTGGCCAGATCCGAG 4667
DB 261 MYSGRRSRQRERFERKRLRGKISPPSYARSDPTDYPKRSPESSSRSRSPPTP 320
QY 4668 AGACGGTTCAACAGCTTGGTACAGATCGAGGCTCCGCGGATTTCTACTGCTTGC 4727
DB 321 GREKTFITSPGSDDEPMAAAMAAASGVTTGKPPAPQPGGAPAGRNASARRSSSS 380
QY 4728 CAACGCCGCTTGGCGGACATGTCGTTGGGTTCCGCACT-TCGCAAGAACGAGAG 4786
DB 381 SSSSSASRTSSRSRSGGYYRSGRHARSRSWSRSRSPSSSRSPSSSRGR 440
QY 4787 CGGAGTGAAGCTGCACTAGTGAAGCCATGAGTGAAGTGGTGGGGAGGATTAAG 4846
DB 441 RHSGGSRDGHYRSRPARGGYGRRRSRSHSGDYYRRGRLRHSSSRSSWSL 500
QY 4847 GTCCGGCGGAGACGCGGCTGTGAGAGTTCCCTCGCAACAGCAAAATCGGTTTGC 4906
DB 501 SPSSRSRLTRSHSPSPSGRSRSRSPSPSPAREKLTLPAAAPVGEKLTKEPBA 560
QY 4907 AG 4908
DB 561 AG 562

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RESULT 14
US-10-158-790-10
; Sequence 10, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:

; CURRENT FILING DATE: 2002-05-06
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 10
 ; LENGTH: 594
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-140-472-10

Query Match 0.6%; Score 40.4; DB 13; Length 594;
 Best Local Similarity 8.1%; Pred. No. 0.24;
 Matches 44; Conservative 194; Mismatches 303; Indels 1; Gaps 1;

QY 4368 GGAGAGATCCGCTTGATCAGCAGACCGCTTCAATGCGGAGTGAAGCGGTTGACG 4427
 DB 21 KRAERREYKIKKDPAPLOVHGRACKVHLSVALAASPVMMWQGTNNMIDRF 80
 QY 4428 GCGTCTCATGCTCGAAGCTCAATGCTTCAACAGAGATCCGTCACCTGCCGTTGAG 4487
 DB 81 DVRAHLHIPIYTPPLTLTISPEQSDERKCNRYRGLVNDPAGISEBQCLVQIYIDE 140
 QY 4488 CTGTGCTTAACGCGGCACATCTGTGCTGATGCGCGGCAACAATCCACAGATTGTC 4547
 DB 141 LYGGLRSEDEKTKLAEKKASIGTYEDSTVAEVEKAERPEEESAABEESNDEDEV 200
 QY 4548 CGCATATCCCGGCGCAAGCAGACGATGAACAGCGGTCATGAGTTTGAAGCGCGG 4607
 DB 201 IPDIDVEVDVLENOBOVADLNKQATTYGMADGDFVRLMKDKEBAIKAKALEEKA 260
 QY 4608 CTGAACGCTCGTTTGCAGCAGATCAGACGCTCTCTTAAAGTTGGCCAGATCCGAG 4667
 DB 261 MYSGRRSRQRREFREKRLRGKISPSYARSDPTDYKRSPESSSESRSRSPPTP 320
 QY 4668 AGACGCTTCAACGCTTGCGGTACAGATCGAGCTCCGCGGCTTCTACTGCTTGGC 4727
 DB 321 GREKITFTITSPGSDDEMAAAAAAASGVTTGKPPAPPOGPAFGPGRNARSRRSSS 380
 QY 4728 CAAGCCCGGTGTTGGGAGCATGTCGGTGGGTTCCGCACT-TCGCAAGACGACGAG 4786
 DB 381 SSSSASRTSSRSRSSRSRRGGYRSGRHARSRSRSRSRRSRSSRSRGR 440
 QY 4787 CGCAGTGAAGCTGCACTAGTGAAGCCCATGAGTGCATGTCGCGGCGAGATTACG 4846
 DB 441 RHSGGSRDGHRYSPARRRGYGRRRRSRSHSGDYRRRGGLRHSSRSRSM 500
 QY 4847 GTGCGGCGGAACCGGCGTGTGAGCTTCCCTCGCAACAGCAATCCGCTTGTGC 4906
 DB 501 SPSRSLTRSRSHSPSPQSRSRSRSPSPSPAPAREKLTTPAASPVEKLTKEBPA 560
 QY 4907 AG 4908
 DB 561 AG 562

RESULT 12
 US-10-141-761-10
 ; Sequence 10, Application US/10141761
 ; Publication No. US20030148432A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel

; APPLICANT: Matanabe, Colin X
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P330R1C198
 ; CURRENT APPLICATION NUMBER: US/10141,761
 ; CURRENT FILING DATE: 2002-05-08
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 10
 ; LENGTH: 594
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-141-761-10

Query Match 0.6%; Score 40.4; DB 13; Length 594;
 Best Local Similarity 8.1%; Pred. No. 0.24;
 Matches 44; Conservative 194; Mismatches 303; Indels 1; Gaps 1;

QY 4368 GGAGAGATCCGCTTGATCAGCAGACCGCTTCAATGCGGAGTGAAGCGGTTGACG 4427
 DB 21 KRAERREYKIKKDPAPLOVHGRACKVHLSVALAASPVMMWQGTNNMIDRF 80
 QY 4428 GCGTCTCATGCTCGAAGCTCAATGCTTCAACAGAGATCCGTCACCTGCCGTTGAG 4487
 DB 81 DVRAHLHIPIYTPPLTLTISPEQSDERKCNRYRGLVNDPAGISEBQCLVQIYIDE 140
 QY 4488 CTGTGCTTAACGCGGCACATCTGTGCTGATGCGCGGCAACAATCCACAGATTGTC 4547
 DB 141 LYGGLRSEDEKTKLAEKKASIGTYEDSTVAEVEKAERPEEESAABEESNDEDEV 200
 QY 4548 CGCATATCCCGGCGCAAGCAGACGATGAACAGCGGTCATGAGTTTGAAGCGCGG 4607
 DB 201 IPDIDVEVDVLENOBOVADLNKQATTYGMADGDFVRLMKDKEBAIKAKALEEKA 260
 QY 4608 CTGAACGCTCGTTTGCAGCAGATCAGACGCTCTCTTAAAGTTGGCCAGATCCGAG 4667
 DB 261 MYSGRRSRQRREFREKRLRGKISPSYARSDPTDYKRSPESSSESRSRSPPTP 320
 QY 4668 AGACGCTTCAACGCTTGCGGTACAGATCGAGCTCCGCGGCTTCTACTGCTTGGC 4727
 DB 321 GREKITFTITSPGSDDEMAAAAAAASGVTTGKPPAPPOGPAFGPGRNARSRRSSS 380
 QY 4728 CAAGCCCGGTGTTGGGAGCATGTCGGTGGGTTCCGCACT-TCGCAAGACGACGAG 4786
 DB 381 SSSSASRTSSRSRSSRSRRGGYRSGRHARSRSRSRSRRSRSSRSRGR 440
 QY 4787 CGCAGTGAAGCTGCACTAGTGAAGCCCATGAGTGCATGTCGCGGCGAGATTACG 4846
 DB 441 RHSGGSRDGHRYSPARRRGYGRRRRSRSHSGDYRRRGGLRHSSRSRSM 500
 QY 4847 GTGCGGCGGAACCGGCGTGTGAGCTTCCCTCGCAACAGCAATCCGCTTGTGC 4906
 DB 501 SPSRSLTRSRSHSPSPQSRSRSRSPSPSPAPAREKLTTPAASPVEKLTKEBPA 560
 QY 4907 AG 4908
 DB 561 AG 562

RESULT 13
 US-10-142-885-10
 ; Sequence 10, Application US/10142885
 ; Publication No. US20030157604A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.


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; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235765
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(612)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-235765
```

Query Match 0.6%; Score 42; DB 14; Length 612;
Best Local Similarity 53.8%; Pred. No. 0.075; Matches 84; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

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QY 367 AGCGTACCAATTTCCGAGGAGTTTCTGCTGCATTAATTTTCTTCTGTAATC 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 347 ARTGTATGCAATCAATGCTATTAATTTCTTAAGCACTGTTGCTGCATCCACACA 288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 GATCATTAAGTTGTTTGTGTTTGTGCTCTGACGATTTGCAACCGTTGATTGCGG 486
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 TTGTATTAAGTTGCTTTTGTGTTTGTTCATTAAGAAATATTTTAAATTTCTTGAGATTCT 228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 487 TATTTGCAAAATACCTCCATATGATGATGATTTT 522
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 227 TCTTTGACCTATTAGTTATTAAGGAGTGTGTTATTTA 192
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RESULT 7

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US-10-027-632-235766/c
; Sequence 235766, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235766
; LENGTH: 612
; TYPE: DNA
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```

; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(612)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-235766
```

Query Match 0.6%; Score 42; DB 14; Length 612;
Best Local Similarity 53.8%; Pred. No. 0.075; Matches 84; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

```

QY 367 AGCGTACCAATTTCCGAGGAGTTTCTGCTGCATTAATTTTCTTCTGTAATC 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 347 ARTGTATGCAATCAATGCTATTAATTTCTTAAGCACTGTTGCTGCATCCACACA 288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 GATCATTAAGTTGTTTGTGTTTGTGCTCTGACGATTTGCAACCGTTGATTGCGG 486
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 TTGTATTAAGTTGCTTTTGTGTTTGTTCATTAAGAAATATTTTAAATTTCTTGAGATTCT 228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 487 TATTTGCAAAATACCTCCATATGATGATGATTTT 522
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 227 TCTTTGACCTATTAGTTATTAAGGAGTGTGTTATTTA 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 8

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US-10-027-632-235767/c
; Sequence 235767, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235767
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(612)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-235767
```

Query Match 0.6%; Score 42; DB 14; Length 612;
Best Local Similarity 53.8%; Pred. No. 0.075; Matches 84; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

```

QY 367 AGCGTACCAATTTCCGAGGAGTTTCTGCTGCATTAATTTTCTTCTGTAATC 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 347 ARTGTATGCAATCAATGCTATTAATTTCTTAAGCACTGTTGCTGCATCCACACA 288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 GATCATTAAGTTGTTTGTGTTTGTGCTCTGACGATTTGCAACCGTTGATTGCGG 486
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 TTGTATTAAGTTGCTTTTGTGTTTGTTCATTAAGAAATATTTTAAATTTCTTGAGATTCT 228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 487 TATTTGCAAAATACCTCCATATGATGATGATTTT 522
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 235765
LENGTH: 612
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(612)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-235765

Query Match 0.6%; Score 42; DB 13; Length 612;
Best Local Similarity 53.8%; Pred. No. 0.075;
Matches 84; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

QY 367 AGCGTACCAATTTCCGAGGAGGTTTCTCGCTGATATTTTCTTCTTCTGATC 426
DB 347 ARTGTATGACATCAATCTATTAATTTTCTTAAGACCTGCTTGTGATCCACACA 288
QY 427 GATCATTAAGTGTGTTTGTGCTCTCGACGATTTGCAACGGTTGATGATTCG 486
DB 287 TTTGATTAAGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 228
QY 487 TATTTGTCAAAATCTCCATATGATTCATTTTGA 522
DB 227 TCTTTGACCTATTAAGTATTAAGGCTGTTGTTATTA 192

RESULT 4

US-10-027-632-235766/c
Sequence 235766, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 235766
LENGTH: 612
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(612)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-235766

Query Match 0.6%; Score 42; DB 13; Length 612;
Best Local Similarity 53.8%; Pred. No. 0.075;
Matches 84; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

QY 367 AGCGTACCAATTTCCGAGGAGGTTTCTCGCTGATATTTTCTTCTTCTGATC 426
DB 347 ARTGTATGACATCAATCTATTAATTTTCTTAAGACCTGCTTGTGATCCACACA 288

QY 427 GATCATTAAGTGTGTTTGTGCTCTCGACGATTTGCAACCGTTGATTCGATTCG 486
DB 287 TTTGATTAAGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 228
QY 487 TATTTGTCAAAATCTCCATATGATTCATTTTGA 522
DB 227 TCTTTGACCTATTAAGTATTAAGGCTGTTGTTATTA 192

RESULT 5

US-10-027-632-235767/c
Sequence 235767, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 235767
LENGTH: 612
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(612)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-235767

Query Match 0.6%; Score 42; DB 13; Length 612;
Best Local Similarity 53.8%; Pred. No. 0.075;
Matches 84; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

QY 367 AGCGTACCAATTTCCGAGGAGGTTTCTCGCTGATATTTTCTTCTTCTGATC 426
DB 347 ARTGTATGACATCAATCTATTAATTTTCTTAAGACCTGCTTGTGATCCACACA 288
QY 427 GATCATTAAGTGTGTTTGTGCTCTCGACGATTTGCAACCGTTGATTCGATTCG 486
DB 287 TTTGATTAAGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 228
QY 487 TATTTGTCAAAATCTCCATATGATTCATTTTGA 522
DB 227 TCTTTGACCTATTAAGTATTAAGGCTGTTGTTATTA 192

RESULT 6

US-10-027-632-235765/c
Sequence 235765, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632

QY 5401 CGGTGAGACGGCTCACGGCATTTGAGGCTATGTTCCCTGGATGACGGGCGCTATTTT 5460
DB 5401 CGGTGAGACGGCTCACGGCATTTGAGGCTATGTTCCCTGGATGACGGGCGCTATTTT 5460
QY 5461 ACGACTGTGAGACGATCGGTTGTTTCCGACGGCTATCGGGGTATCATACGAGACGGT 5520
DB 5461 ACGACTGTGAGACGATCGGTTGTTTCCGACGGCTATCGGGGTATCATACGAGACGGT 5520
QY 5521 AGATGATATGATATTTGGGCTGAGGATATCATGTGGGCTTATCAACCGTGCCTGT 5580
DB 5521 AGATGATATGATATTTGGGCTGAGGATATCATGTGGGCTTATCAACCGTGCCTGT 5580
QY 5581 TTGGCGATGTCTACCTCGACTTGGGCAATATATGATGATCTATCGATGAGGCGTCC 5640
DB 5581 TTGGCGATGTCTACCTCGACTTGGGCAATATATGATGATCTATCGATGAGGCGTCC 5640
QY 5641 TCTATGACACGTCATACAGACCGCTCGAGAAAGCGCTCTGTAAGCTTGATCAATG 5700
DB 5641 TCTATGACACGTCATACAGACCGCTCGAGAAAGCGCTCTGTAAGCTTGATCAATG 5700
QY 5701 CGGTGATCTCTCAGCGAATAGCGCTGATGATTTATTCATAGCGCGCATG 5760
DB 5701 CGGTGATCTCTCAGCGAATAGCGCTGATGATTTATTCATAGCGCGCATG 5760
QY 5761 CCTGCGAATGAAAGCGCGCATGCGCTTTTCTCTTATGAAAGCGCGTGGCAGTC 5820
DB 5761 CCTGCGAATGAAAGCGCGCATGCGCTTTTCTCTTATGAAAGCGCGTGGCAGTC 5820
QY 5821 GTCCGTTTGGGCGCTAAGCGCTGACCGACGGCGGCAACAGCGACCGTCTTATGAC 5880
DB 5821 GTCCGTTTGGGCGCTAAGCGCTGACCGACGGCGGCAACAGCGACCGTCTTATGAC 5880
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DB 5881 GCGTTGCCACACAGACGAGCGCGCTTGTAGAGTGCAGAAATCTGTCGCGGGCGAG 5940
QY 5941 GCTGAAGGTAAACCGCGCTGTGTGTCTACTATGGAATCCAGGTGGGTCATGAA 6000
DB 5941 GCTGAAGGTAAACCGCGCTGTGTGTCTACTATGGAATCCAGGTGGGTCATGAA 6000
QY 6001 TGATGAGATTTGCTGACAGGTGGCGGACGAACTGTCAACGCGCGCGCGGCGAGTGT 6060
DB 6001 TGATGAGATTTGCTGACAGGTGGCGGACGAACTGTCAACGCGCGCGCGGCGAGTGT 6060
QY 6061 GTATGCGGAGGCGCGCTGTGTCTCAACCGTCAATTCCTGCGGCACTCTGAAAC 6120
DB 6061 GTATGCGGAGGCGCGCTGTGTCTCAACCGTCAATTCCTGCGGCACTCTGAAAC 6120
QY 6121 CTCTGCGTTGCTGAGGCTCTTCTGTTGTGGGACCGGTTGATGAGCGGCGGAG 6180
DB 6121 CTCTGCGTTGCTGAGGCTCTTCTGTTGTGGGACCGGTTGATGAGCGGCGGAG 6180
QY 6181 GACATTTATCGTTTATCGAGGCTGAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 6240
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QY 6241 TCCGCAATTTGGAATGATTTGCGGCGACTGACAGTGCACCGCTGTTCAACCTTC 6300
DB 6241 TCCGCAATTTGGAATGATTTGCGGCGACTGACAGTGCACCGCTGTTCAACCTTC 6300
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QY 6361 AGGACACTGCGACACAGGCGCATGAACTTTGTTGCGGCTCAGGATTTGCTGCGGT 6420
DB 6361 AGGACACTGCGACACAGGCGCATGAACTTTGTTGCGGCTCAGGATTTGCTGCGGT 6420
QY 6421 GATTAATTTGGAGGTGCTGCGGCTGTCAGGCGGATATCGAATTTGGCCAGCTTTGTT 6480
DB 6421 GATTAATTTGGAGGTGCTGCGGCTGTCAGGCGGATATCGAATTTGGCCAGCTTTGTT 6480
QY 6481 GCTGAATGCCAGCTCTACGATGACGACATTCGAGGAGGCTCGGATTTAGCTCTGTAC 6540

DB 6481 GCTGAATGCCAGCTCTACGATGACGACATTCGAGGAGGCTCGGATTTAGCTCTGTAC 6540
QY 6541 CATGAGACGCGATCAAGTTGCGCTGCTGCTTGAAGCGCTATGCTGTCTCGAAGCAACG 6600
DB 6541 CATGAGACGCGATCAAGTTGCGCTGCTGCTTGAAGCGCTATGCTGTCTCGAAGCAACG 6600
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DB 6601 CGGCGGCTTGTGCAAAAGCTTAATACGTTGCGAGTTGACAGTCGCGCGGAGCGGCA 6660
QY 6661 AGAGCGGCTGTCAACGCGCAGAGTGCAGATGCGGAAACCGCTATGCGCATTTGCTGCG 6720
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DB 6721 CACTGAAGTCTCTCTGATGATCTTCATCATCGGCAACACTGGAAGCAGCGCTGGCAT 6780
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DB 6781 GTAGGCGGCGACCGCGCATATGCTGAGGAGCGAAGCTGCGGAGCTGGGCTTGGAGTTA 6840
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DB 6841 AGTTCAGCAACGAGGCGGAGACACTATGAAAGCTTCTGAGGCGGCTTCTGCGCTTTA 6900
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DB 6901 TCACGAAAAACAGATGCACTTCTCGAAGACTGCAAAAAAGTCCGAAAGCTCTGCG 6960
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DB 6961 TGTGTGACGCGCTGCTGATGTCGGAATCTTCTGCTGAGAGAGGATGCTGACG 7020
QY 7021 TCTACTATCGGCGAGCGGCGCATCTATTCATCGAGTTGAGCGGTGCAAGGTGACACAC 7080
DB 7021 TCTACTATCGGCGAGCGGCGCATCTATTCATCGAGTTGAGCGGTGCAAGGTGACACAC 7080
QY 7081 GGACCATGTAAGTACTGCTGTTCTCGACGACCGTCACTTCAATCAAGATGCAAGACG 7140
DB 7081 GGACCATGTAAGTACTGCTGTTCTCGACGACCGTCACTTCAATCAAGATGCAAGACG 7140
QY 7141 CG 7142
DB 7141 CG 7142

RESULT 3
US-10-027-632-235765/C
Sequence 235765, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027, 632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09

Db 3181 GCATGCAAACTTGAAAGAGGGGCAAGGCCAGTATTTGTCGAATCTGCGCGCTG 3240
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 Db 3721 TGTGTGAGCAAGAAAGTTTCCGAAATCGGGGTTTTTATTTCCGTTTTTCACTTTGGTG 3780
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 Db 3781 AATTGACAGCGGACTTGCAGATTTGGGCTTGGACGCTGACGTCAGCAACGATTGATTAAGC 3840
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Db 1021 AGGCATGTGCGAGTGGCGCATCATCGAAACCGGTGGGCTTTGAAAGACCCGCAATTTGATCC 1080
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Db 1081 TTTGACGGTAAAGCTGTGCATCATGTGCCACAGGCGATGGGATTATCACTTGCTCAAGTCC 1140
Qy 1141 CATGCATCGATCATATTTATCTTGATGGGAGAACGCTTAAACCCCGAGACCTTGAAACAAAT 1200
Db 1141 CATGCATCGATCATATTTATCTTGATGGGAGAACGCTTAAACCCCGAGACCTTGAAACAAAT 1200
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Db 1201 GGACACAGATTTGTGCGAGAGAGCTGTTCCGTCGAATTTTCAAGAGCCGCAACTCTCCG 1260
Qy 1261 ACCGAAATATGATTTTCCAAAGTTATGATGCGCTGACAGGCTTCGAATTCATTAATCTCGGC 1320
Db 1261 ACCGAAATATGATTTTCCAAAGTTATGATGCGCTGACAGGCTTCGAATTCATTAATCTCGGC 1320
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Qy 1441 CGAGCATCTGCGAAAGCGCGTCCATCCGAGAGAGCGCGACACCCCATGGAATTTCAAGT 1500
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Db 1501 GGTGTGCGCGCATGAGATTTGAGATGCAAGACTGCGGATATCACTAATGTTTCGCA 1560
Qy 1561 TCATCGGCTCGATGCTATGGAATAGCGTCACTCATTTGAAAGCACTGCAAGAGCAAG 1620
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Db 1621 CTGAGTGTGCTGCGCGCATCGGTCAAAACCGTTGCGCTTTGCTTATTCATTAATGTCG 1680
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Db 1741 TCTTGGGCAATATCCATGCGCAAGAGTTTGGCTGCGAAATCTCTGCGCTCGATTTGAG 1800
Qy 1801 TGAAAACCTTTTCTGTGCGGAAAGCATAGTTGAGAGCGCTTGAAGCTTCGATTCAT 1860
Db 1801 TGAAAACCTTTTCTGTGCGGAAAGCATAGTTGAGAGCGCTTGAAGCTTCGATTCAT 1860
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Db 1861 CGAGTCCGCGATGTGAGCTTTGTGCTCAACAGACGAAACCAAGATTTGAATGTCG 1920
Qy 1921 GCCCGCTTCTCAACTGATCTTTGAAAGATGATCCCGCTCTCAAAAGACCTCTGACCG 1980
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Db 1981 CGGACAGCTTTTCTTACCGATGTTGAACCTTTGCGGATACATTCAGCCATTTGCCAAGA 2040
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Db 2041 AATCCCGCGCGAGACTGGGATTTGGCTGCTCTGTGCTGATGAGGCTGATGTTGAC 2100
Qy 2101 AAACCAACCGCGCTCGAGCCATCGAAGCATGTTGATGCTGATCTTTGATGCTCGC 2160

2101 AAACCAACCGCGCTCGAGCCATCGAAGCATGTTGATGCTGATCTTTGATGCTCGC 2160
Db 2161 CGTGATCTCTCTCGCAAGAGGAGGATCCAGTGTGGGTGATTAAGGATGGGTGACG 2220
Qy 2161 CGTGATCTCTCTCGCAAGAGGAGGATCCAGTGTGGGTGATTAAGGATGGGTGACG 2220
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Qy 2221 CACTGATCTGCAATTTGCGAGCAAGAAATCCAAATTAATGACGATCCAAATTTG 2280
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Qy 2761 TCTGCGGAGTTTGAAGCATACACATGCGGATCAGGCAAGAGGAGCTACCGCAATC 2820
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Db	6541	CATGAGACCGCATCAAGTTCCGCTCTGTCATGACGGCATGAGTGTCTCGGAAGCAACG	6600
Qy	6541	CATGAGACCGCATCAAGTTCCGCTCTGTCATGACGGCATGAGTGTCTCGGAAGCAACG	6600
Db	6541	CATGAGACCGCATCAAGTTCCGCTCTGTCATGACGGCATGAGTGTCTCGGAAGCAACG	6600
Qy	6601	CGGCGGCTTCGTGCACAGCTTAATCACTTTCGACAGTTCACAGATGCGGCCGAGCGCA	6660
Db	6601	CGGCGGCTTCGTGCACAGCTTAATCACTTTCGACAGTTCACAGATGCGGCCGAGCGCA	6660
Qy	6661	AGAGCGGCTGTCAAGCTTAATCACTTTCGACAGTTCACAGATGCGGCCGAGCGCA	6720
Db	6661	AGAGCGGCTGTCAAGCTTAATCACTTTCGACAGTTCACAGATGCGGCCGAGCGCA	6720
Qy	6721	CACCTAAGAGTGTCTCTGGAATGCTCATCATTCGCGAACAACCTGAGAGCAGCGCTGGCATA	6780
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Qy	6781	GTAGGCGACGACCGCGCCATTAAGTGTGGAGCGAAGCTCGGACTGGGGTTGCGAGGTTA	6840
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Db	6841	AGTTGAGAGCAAGGGGGGAGACACTAATGAAAGCTTGTTAGGCGCGTTGCTCGCTTTA	6900
Qy	6901	TCACAGAAAAACAGATGCACTTTCGAAAGAGACTGCAAAAAAGTCCGAAAGGCTCTGGC	6960
Db	6901	TCACAGAAAAACAGATGCACTTTCGAAAGAGACTGCAAAAAAGTCCGAAAGGCTCTGGC	6960
Qy	6961	TGTGTGACCGCGCTCGGTGATTCGCGAACAATTTCTTGCGCTTGAGAGACGAGCTATCGACG	7020
Db	6961	TGTGTGACCGCGCTCGGTGATTCGCGAACAATTTCTTGCGCTTGAGAGACGAGCTATCGACG	7020
Qy	7021	TCTACTATCGGGAGCGGGCCATCTTAATTCATCGAGTTGAGGGGTGGAGAGTGCACACAC	7080
Db	7021	TCTACTATCGGGAGCGGGCCATCTTAATTCATCGAGTTGAGGGGTGGAGAGTGCACACAC	7080
Qy	7081	GGACCCCATGTGAAGTACTGTGTTCTCGACGACCGTGACCCCTTATCATCAAGATGACGAACG	7140
Db	7081	GGACCCCATGTGAAGTACTGTGTTCTCGACGACCGTGACCCCTTATCATCAAGATGACGAACG	7140
Qy	7141	CG 7142	
Db	7141	CG 7142	

Query Match	Similarity	100.0%	Score 7142:	DB 9:	Length 7142:
Best Local	Similarity	100.0%	Prod. No. 0:		
Matches 7142:	Conservative	0:	Mismatches	0:	Indels
					Gaps 0:
Qy	1	CGCGTAAAGACACAGACAGTCTCCGTAAGACCATTAAGAGCTTTTAGAGACCCAAACGCA	60		
Db	1	CGCGTAAAGACACAGAGAGTCTCCGTAAGACCATTAAGAGCTTTTAGAGACCCAAACGCA	60		
Qy	61	TAGAGAGCCGCTTTCTAAAGCTGCTAGACAGTTGGTGCTTAATTCCTTGGTAGCGTAACAT	120		
Db	61	TAGAGAGCCGCTTTCTAAAGCTGCTAGACAGTTGGTGCTTAATTCCTTGGTAGCGTAACAT	120		
Qy	121	TGATGCAATATACAAAAGTGAATCTGGCCCTAACAAAGACCCGATCCGCTCTTAC	180		
Db	121	TGATGCAATATACAAAAGTGAATCTGGCCCTAACAAAGACCCGATCCGCTCTTAC	180		
Qy	181	TAGTCGCGCAACCTTAGCTGTAAAGAAATTTAGATGGCGGTTGTCAATCCACATCGATAC	240		
Db	181	TAGTCGCGCAACCTTAGCTGTAAAGAAATTTAGATGGCGGTTGTCAATCCACATCGATAC	240		
Qy	241	GTTTGCTGCGGCTTGTGTTCTCAACCACTCATCTAATTTCCGAGAAATTTCCGTATGGTC	300		
Db	241	GTTTGCTGCGGCTTGTGTTCTCAACCACTCATCTAATTTCCGAGAAATTTCCGTATGGTC	300		
Qy	301	AGCCAAACCAAGTCTGCGATGATGATGCCCGCAATACACGGCGGAGAGTCGCGGATCAT	360		
Db	301	AGCCAAACCAAGTCTGCGATGATGATGCCCGCAATACACGGCGGAGAGTCGCGGATCAT	360		
Qy	361	CGCGAAGCGTCACCAATTTCCGAGAGAGGTTTCTCGCGCATAAATTTTCTTCTCC	420		
Db	361	CGCGAAGCGTCACCAATTTCCGAGAGAGGTTTCTCGCGCATAAATTTTCTTCTCC	420		
Qy	421	TGAATGATCATTAAGTTGTGTTTTTGTGCTCGACGTAATTTGCAACCGTTGATTCG	480		
Db	421	TGAATGATCATTAAGTTGTGTTTTTGTGCTCGACGTAATTTGCAACCGTTGATTCG	480		
Qy	481	ATTGCGATTTGTCAAATACTCCATATGATGATTTTAAAGACAAATAGGCTCA	540		
Db	481	ATTGCGATTTGTCAAATACTCCATATGATGATTTTAAAGACAAATAGGCTCA	540		
Qy	541	CATTGTCAGCAATAGACTCTGGCAAAACCCCAATCGCTAAATAGAGTGTGTTGCATGG	600		
Db	541	CATTGTCAGCAATAGACTCTGGCAAAACCCCAATCGCTAAATAGAGTGTGTTGCATGG	600		
Qy	601	ATAACAAAGTTGCGAAGATGTCGAAAGTGAAGAGGCTCCATCAAGGCGACCTTCAAGG	660		
Db	601	ATAACAAAGTTGCGAAGATGTCGAAAGTGAAGAGGCTCCATCAAGGCGACCTTCAAGG	660		
Qy	661	CTGCTGTTCTGAAGTGCAGAACCGAAGGTGCACATCGAGAGTACGCCGTACAGGCTGCGTCG	720		
Db	661	CTGCTGTTCTGAAGTGCAGAACCGAAGGTGCACATCGAGAGTACGCCGTACAGGCTGCGTCG	720		
Qy	721	CTTAAGTGAACATCCGCGGAGTGGGCAAAAGTACCGGCACCTAATGCTCTCGCTTTCAA	780		
Db	721	CTTAAGTGAACATCCGCGGAGTGGGCAAAAGTACCGGCACCTAATGCTCTCGCTTTCAA	780		
Qy	781	CGGAGATTTTCGATGAGACTTTCGTCAACGATTCGTAATCGACCGCTCTTTCACCTCCG	840		
Db	781	CGGAGATTTTCGATGAGACTTTCGTCAACGATTCGTAATCGACCGCTCTTTCACCTCCG	840		
Qy	841	CTACTACAGCTTCGACGCTTATCTAATTCGCGACATTCGACATTCGACGCGAAGATCT	900		
Db	841	CTACTACAGCTTCGACGCTTATCTAATTCGCGACATTCGACATTCGACGCGAAGATCT	900		
Qy	901	CATCACTCAAAATCGCTAATTTTGGGACATTTGGTGCATTCATGACGCGAAGATCT	960		
Db	901	CATCACTCAAAATCGCTAATTTTGGGACATTTGGTGCATTCATGACGCGAAGATCT	960		
Qy	961	GGTAGAGCGTGTGAGACGCTATCCGATTAACATCCGAGAAAGTGGCCGACGAATTCGA	1020		
Db	961	GGTAGAGCGTGTGAGACGCTATCCGATTAACATCCGAGAAAGTGGCCGACGAATTCGA	1020		

Db 4321 GATCTTCAGTACGAGATTGCGGTTGCAAAAGCAAGTCTAGCTTCCGAGAGAGATCCG 4380
 Qy 4381 TTTGATATACCAAGAGCTTCAATCCGCGAGTGAAGCGGGTTGCAAGCGCTCTATGCTC 4440
 Db 4381 TTTGATATACCAAGAGCTTCAATCCGCGAGTGAAGCGGGTTGCAAGCGCTCTATGCTC 4440
 Qy 4441 GAAGTATACCAATGCTTCAACAGAGATCCGCTCACTGCGCGTGTAGCTGTTCTTAAG 4500
 Db 4441 GAAGTATACCAATGCTTCAACAGAGATCCGCTCACTGCGCGTGTAGCTGTTCTTAAG 4500
 Qy 4501 CGGCGACATCTGTGTGATGCGGCGCAACATCTCAAGATTTGCGGCAATCCCGG 4560
 Db 4501 CGGCGACATCTGTGTGATGCGGCGCAACATCTCAAGATTTGCGGCAATCCCGG 4560
 Qy 4561 CGGCGACATCTGTGTGATGCGGCGCAACATCTCAAGATTTGCGGCAATCCCGG 4620
 Db 4561 CGGCGACATCTGTGTGATGCGGCGCAACATCTCAAGATTTGCGGCAATCCCGG 4620
 Qy 4621 TTTGACGAGATCAGACATCTCTCTTAAGTTGGCGACATCCGACGAGCGGTTCAACA 4680
 Db 4621 TTTGACGAGATCAGACATCTCTCTTAAGTTGGCGACATCCGACGAGCGGTTCAACA 4680
 Qy 4681 GCTTGGGTAACAGAAATCGAGGCTCCGCGAGTTTCTACTGCTTGGCGAACGCGCTGT 4740
 Db 4681 GCTTGGGTAACAGAAATCGAGGCTCCGCGAGTTTCTACTGCTTGGCGAACGCGCTGT 4740
 Qy 4741 GCGGACATCTGTGTGATGCGGCGCAACATCTCAAGATTTGCGGCAATCCCGG 4800
 Db 4741 GCGGACATCTGTGTGATGCGGCGCAACATCTCAAGATTTGCGGCAATCCCGG 4800
 Qy 4801 GCAATCTAGTGAAGCCATCTGATGAGTGTGCGGCGAGATTAAGGTCGCGCGGAAC 4860
 Db 4801 GCAATCTAGTGAAGCCATCTGATGAGTGTGCGGCGAGATTAAGGTCGCGCGGAAC 4860
 Qy 4861 GCGGTCGAGGCTTCCCTCGCAACAGCAAAATCGCGTTGTGCGAGGCGAGCGGCTG 4920
 Db 4861 GCGGTCGAGGCTTCCCTCGCAACAGCAAAATCGCGTTGTGCGAGGCGAGCGGCTG 4920
 Qy 4921 CGCATCTGATGAGTCACTATTAACGTGATACAGCGGCGTATGTTTCAAGAGCAAG 4980
 Db 4921 CGCATCTGATGAGTCACTATTAACGTGATACAGCGGCGTATGTTTCAAGAGCAAG 4980
 Qy 4981 AAACACCGATCTTGAATTAACCGGCTCCGTTGTTGATTTCCGTCGCGCGTCAAGC 5040
 Db 4981 AAACACCGATCTTGAATTAACCGGCTCCGTTGTTGATTTCCGTCGCGCGTCAAGC 5040
 Qy 5041 GAGAAATTCGATTCGAAATTCGCAACATCTAGAGTGCCTGAGCATATTTTCAAGCGT 5100
 Db 5041 GAGAAATTCGATTCGAAATTCGCAACATCTAGAGTGCCTGAGCATATTTTCAAGCGT 5100
 Qy 5101 ATGACCCCGTAACTTGTGTCGAGTGTGTTTCTGAGTCCGCTATCGAATTAACAG 5160
 Db 5101 ATGACCCCGTAACTTGTGTCGAGTGTGTTTCTGAGTCCGCTATCGAATTAACAG 5160
 Qy 5161 ATGACCCCGTAACTTGTGTCGAGTGTGTTTCTGAGTCCGCTATCGAATTAACAG 5220
 Db 5161 ATGACCCCGTAACTTGTGTCGAGTGTGTTTCTGAGTCCGCTATCGAATTAACAG 5220
 Qy 5221 TTTCAACCGATCTCAAGCTGACCGCGCTATCGAGCAAGGCTGATCCAGCTTCCAG 5280
 Db 5221 TTTCAACCGATCTCAAGCTGACCGCGCTATCGAGCAAGGCTGATCCAGCTTCCAG 5280
 Qy 5281 TTTCCGTTCTTAAAGAGCGCGATCAATTTTGTATCTTGTGTCGCTCTGATCCGCGG 5340
 Db 5281 TTTCCGTTCTTAAAGAGCGCGATCAATTTTGTATCTTGTGTCGCTCTGATCCGCGG 5340
 Qy 5341 TTTGAGATGTTGAGAGCGGAAATTCAGGATGACGATCTTCTTAAAGAGATGATCTT 5400
 Db 5341 TTTGAGATGTTGAGAGCGGAAATTCAGGATGACGATCTTCTTAAAGAGATGATCTT 5400
 Qy 5401 CGGTTGAGCGGCTCAAGGATTCGAGCTTATGTTTCCCTGAGTGAAGCGGCGTATTAAT 5460
 Db 5401 CGGTTGAGCGGCTCAAGGATTCGAGCTTATGTTTCCCTGAGTGAAGCGGCGTATTAAT 5460

Db 5401 CGGTTGAGCGGCTCAAGGATTCGAGCTTATGTTTCCCTGAGTGAAGCGGCGTATTAAT 5460
 Qy 5461 ACGACTGAGCAGCATCGGTTGTTTCCGAGGCTATCCGCGGATCTACAGAGCGGTC 5520
 Db 5461 ACGACTGAGCAGCATCGGTTGTTTCCGAGGCTATCCGCGGATCTACAGAGCGGTC 5520
 Qy 5521 AGATCATATGATATTTCCGCTGAGGATATCATGTGCGTTTAAACCGCTGCTGTC 5580
 Db 5521 AGATCATATGATATTTCCGCTGAGGATATCATGTGCGTTTAAACCGCTGCTGTC 5580
 Qy 5581 TTTGCGATGTTTACCTGACCTTGGCAATATTAAGTACTCTATCGATGATGCGGCTCC 5640
 Db 5581 TTTGCGATGTTTACCTGACCTTGGCAATATTAAGTACTCTATCGATGATGCGGCTCC 5640
 Qy 5641 TCTATGACAGTCTATACAGAGCGGCTCTGAGAGAGCGGCTCTGATGATGATGATG 5700
 Db 5641 TCTATGACAGTCTATACAGAGCGGCTCTGAGAGAGCGGCTCTGATGATGATGATG 5700
 Qy 5701 CGGTCATCTCCAGCGATACCGGTTGATGATTTAAATCCATAGGCGGAGAGGAGATG 5760
 Db 5701 CGGTCATCTCCAGCGATACCGGTTGATGATTTAAATCCATAGGCGGAGAGGAGATG 5760
 Qy 5761 CTTGCGAACTGAGAGAGCGGCAATCCGTTTCTTGAATGAACCGCTGCGCAGTC 5820
 Db 5761 CTTGCGAACTGAGAGAGCGGCAATCCGTTTCTTGAATGAACCGCTGCGCAGTC 5820
 Qy 5821 GTCGTTTGGGCGGTAAGCGCTGACCGAGGCGGCGCAAGCGGCTGTTTATGCG 5880
 Db 5821 GTCGTTTGGGCGGTAAGCGCTGACCGAGGCGGCGCAAGCGGCTGTTTATGCG 5880
 Qy 5881 GCGTTGCAACAGAGAGAGCGGCTTGAAGTGAAGAAATGTTTCCGCGGCGGAG 5940
 Db 5881 GCGTTGCAACAGAGAGAGCGGCTTGAAGTGAAGAAATGTTTCCGCGGCGGAG 5940
 Qy 5941 GCTGAAAGTAAAGCGCGCTTGTGTGCTACTATGAATTCAGAGTGGTCCATGA 6000
 Db 5941 GCTGAAAGTAAAGCGCGCTTGTGTGCTACTATGAATTCAGAGTGGTCCATGA 6000
 Qy 6001 TGAATGATTTGCTGACAGGAGGCGAGCAAGCTGTCAAGGCGGCGGCGAGTGT 6060
 Db 6001 TGAATGATTTGCTGACAGGAGGCGAGCAAGCTGTCAAGGCGGCGGCGAGTGT 6060
 Qy 6061 GTATCGCAAGAGCGGCGGCTGATCAACCGTATTCGCTGCGGCACTTGAAGC 6120
 Db 6061 GTATCGCAAGAGCGGCGGCTGATCAACCGTATTCGCTGCGGCACTTGAAGC 6120
 Qy 6121 CTGCGCTTCCGTAAGCTCTTCCGTTGTGCGGCAAGGCTTCAAGAGCGGCGG 6180
 Db 6121 CTGCGCTTCCGTAAGCTCTTCCGTTGTGCGGCAAGGCTTCAAGAGCGGCGG 6180
 Qy 6181 GACATTATCGTTATCGAGGAGTGTGTTTCAACAGGCGGCTGAGAGAGGCTT 6240
 Db 6181 GACATTATCGTTATCGAGGAGTGTGTTTCAACAGGCGGCTGAGAGAGGCTT 6240
 Qy 6241 TCCGCAATTTGGAATGATGTTGCGGCGATGCAACCGCTGCTGTTCAACCTCC 6300
 Db 6241 TCCGCAATTTGGAATGATGTTGCGGCGATGCAACCGCTGCTGTTCAACCTCC 6300
 Qy 6301 CGAAATCTGATGTTGCGGCGATGTTGTTGCGGCGATGCAACCGCTGCTGTTCAAC 6360
 Db 6301 CGAAATCTGATGTTGCGGCGATGTTGTTGCGGCGATGCAACCGCTGCTGTTCAAC 6360
 Qy 6361 AGGACATGCGACAGAGCGGCAATGGAATGTTTGGCGGCGATGTTGCGGCGGTT 6420
 Db 6361 AGGACATGCGACAGAGCGGCAATGGAATGTTTGGCGGCGATGTTGCGGCGGTT 6420
 Qy 6421 GATGATGAGAGTGTGCGGCTGTGAGGCGGATATGAAATGAGGCTGTTG 6480
 Db 6421 GATGATGAGAGTGTGCGGCTGTGAGGCGGATATGAAATGAGGCTGTTG 6480
 Qy 6481 GCTGAATGCCAGCTCTACGATGACGATTTGCGGAGAGGCTGGAATGAGCTGTGAC 6540
 Db 6481 GCTGAATGCCAGCTCTACGATGACGATTTGCGGAGAGGCTGGAATGAGCTGTGAC 6540

OY	2161	GGTCATCTCCCTCGAGAAAGCAGGGAGTCCAGTTGGTGGGTAAAGGATGGGGTGCAGC	2220
Db	2161	CGTCATCTCTCCGAGAAAGCAGGGAGTCCAGTTGGTGGGTAAAGGATGGGGTGCAGC	2220
OY	2221	CACGTATCCTGCAATTTGCGAGACAGAAATCTCAATTTATATATGACGATCCAATTGAATTTG	2280
Db	2221	CACGTATCCTGCAATTTGCGAGACAGAAATCTCAATTTATATATGACGATCCAATTTGAATTTG	2280
OY	2281	GCGGGTTGGAGGATATCAAAAGCTATCCCGAACCCATGGAATTCGAAGCGTNGAAACGCG	2340
Db	2281	GCGGGTTGGAGGATATCAAAAGCTATCCCGAACCCATGGAATTCGAAGCGTNGAAACGCG	2340
OY ^T	2341	GCACCGCAACGGAATTTGGTCAAGCCGCTCCCGGAGCTGGCAGCTGCAATCACTGAGAC	2400
Db	2341	GCACCGCAACGGAATTTGGTCAAGCCGCTCCCGGAGCTGGCAGCTGCAATCACTGAGAC	2400
OY	2401	GAGCTCATGAACAGCGGCTCGTTCAACACCTTCAACGCAAAACACTGTCGATTCACCCGAG	2460
Db	2401	GAGCTCATGAACAGCGGCTCGTTCAACACCTTCAACGCAAAACACTGTCGATTCACCCGAG	2460
OY	2461	TCAGGAGATACCTTTGGTTTGGGAACTCTATGCGCGAGAAACGCGCGGTCAATCGCTGAA	2520
Db	2461	TCAGGAGATACCTTTGGTTTGGGAACTCTATGCGCGAGAAACGCGCGGTCAATCGCTGAA	2520
OY	2521	ATCGGACTTTCGAGTCTCTCGCGCATATATAGCTTTGACAGGCGCTTCTCAGCGTTTGCA	2580
Db	2521	ATCGGACTTTCGAGTCTCTCGCGCATATATAGCTTTGACAGGCGCTTCTCAGCGTTTGCA	2580
OY	2581	CCTTGTTGTCACATATGAGACAGATCGAATGGCAGATGGCTCGTTGCAACCGGAGTCT	2640
Db	2581	CCTTGTTGTCACATATGAGACAGATCGAATGGCAGATGGCTCGTTGCAACCGGAGTCT	2640
OY	2641	ATCGTTACATATGTCGTCAATCACGAACTTGAAGCAATCAGACCGGTGATTTCAAGCTGG	2700
Db	2641	ATCGTTACATATGTCGTCAATCACGAACTTGAAGCAATCAGACCGGTGATTTCAAGCTGG	2700
OY	2701	ACATGAGCAAAACTCGCTATTCGGTCAGAGTGGGGCTTTCAGCGGGCTATATTCACGTTTGGA	2760
Db	2701	ACATGAGCAAAACTCGCTATTCGGTCAGAGTGGGGCTTTCAGCGGGCTATATTCACGTTTGGA	2760
OY	2761	TCGCGGGGATTTGAAGTCATACATATGCGGGTACAGGACAGAGCGGAGCTAACCGCAATC	2820
Db	2761	TCGCGGGGATTTGAAGTCATACATATGCGGGTACAGGACAGAGCGGAGCTAACCGCAATC	2820
OY	2821	TGCTGATCAACACTCAGAGCTCGGCCAATTTCTATTTGACCCCTGCAACGATTCACAGACT	2880
Db	2821	TGCTGATCAACACTCAGAGCTCGGCCAATTTCTATTTGACCCCTGCAACGATTCACAGACT	2880
OY	2881	TCAACACCTTTCTCACGCCCGCCATCAACGATGAGAAAATGCAATCTGTTTCTTGAACGGG	2940
Db	2881	TCAACACCTTTCTCACGCCCGCCATCAACGATGAGAAAATGCAATCTGTTTCTTGAACGGG	2940
OY	2941	AGGAGCACTCCCGTTTATCTCGTCAACGGCAGGCTAAGATATGAGCAGAAAACCAAC	3000
Db	2941	AGGAGCACTCCCGTTTATCTCGTCAACGGCAGGCTAAGATATGAGCAGAAAACCAAC	3000
OY ^F	3001	ATGGGTTCTATCGGACTCGTTTCGAAATACGATCGATGAGTTGGCGAGATGATTTCCCA	3060
Db	3001	ATGGGTTCTATCGGACTCGTTTCGAAATACGATCGATGAGTTGGCGAGATGATTTCCCA	3060
OY	3061	ATGAGGCTGACATATCGTCGTCAACGCTCATACGCGGCTTACATGCACTTCAGGTGCGTCAA	3120
Db	3061	ATGAGGCTGACATATCGTCGTCAACGCTCATACGCGGCTTACATGCACTTCAGGTGCGTCAA	3120
OY	3121	ATGTTTCTGATCAACGATACTGACCTCAATATCGCTTTTCTGAACTTTTGTCTGCTTATCT	3180
Db	3121	ATGTTTCTGATCAACGATACTGACCTCAATATCGCTTTTCTGAACTTTTGTCTGCTTATCT	3180
OY	3181	GCATGCACAATCTGAAAAGAGGGGCAAAAGCGCAAGTATTTGTCGCAATCGTCGCGCTG	3240
Db	3181	GCATGCACAATCTGAAAAGAGGGGCAAAAGCGCAAGTATTTGTCGCAATCGTCGCGCTG	3240

OY	3241	TTTGACATGATGATGGGGTCTACCTGGGCGCTTATTCGGGGTCTCGGTGGCCACCTCCGAG	3300
Db	3241	CTTGATGATGATGATGGGGTCTTACCTGGGCGCTTATTCGGGGTCTCGGTGGCCACCTCCGAG	3300
OY	3301	GTGCAACGCGCGTAAACCAACATTGCTTTCATAGCACTGTCTGCGCTCCGCGCTTTGTG	3360
Db	3301	GTGCAACGCGCGTAAACCAACATTGCTTTCATAGCACTGTCTGCGCTCCGCGCTTTGTG	3360
OY	3361	CTGATGATGATGCTTACTGTGCGGAGGTTTTTTTTCGCCGAGGGAAAACGACAAATTGTGC	3420
Db	3361	CTGATGATGATGCTTACTGTGCGGAGGTTTTTTTTCGCCGAGGGAAAACGACAAATTGTGC	3420
OY	3421	GAACGCTCATACAGAGATCGTGGTATCTATGAGAGGTTAAATCTGCTCTTTCGGGC	3480
Db	3421	GAACGCTCATACAGAGATCGTGGTATCTATGAGAGGTTAAATCTGCTCTTTCGGGC	3480
OY	3481	TGTGCAATTCGCTGGCACTCAAAATTCGATCATATGCTTCTCATCGGCGCTATATCTTG	3540
Db	3481	TGTGCAATTCGCTGGCACTCAAAATTCGATCATATGCTTCTCATCGGCGCTATATCTTG	3540
OY	3541	CTCTCTTCACAAACGCGCTTGCGCTAGCGCAGAAATCTTCCGACCGGAATGAGGTTCACTC	3600
Db	3541	CTCTCTTCACAAACGCGCTTGCGCTAGCGCAGAAATCTTCCGACCGGAATGAGGTTCACTC	3600
OY	3601	GCCAGGATTTGAAGAAGATGTCTTCTCATTTGGGAGGCTGATCTGGTGGGAATCGGGGACG	3660
Db	3601	GCCAGGATTTGAAGAAGATGTCTTCTCATTTGGGAGGCTGATCTGGTGGGAATCGGGGACG	3660
OY	3661	GGCTTTCGCGCTCTTTTATCAACATGCTCGAAAAGGGGTTTCTTGCAATGATGGTGGG	3720
Db	3661	GGCTTTCGCGCTCTTTTATCAACATGCTCGAAAAGGGGTTTCTTGCAATGATGGTGGG	3720
OY	3721	TGTGCGACGAAAGTTTCCGAAATCGCGGTTTTTTATTTTCCGCTTTTCACTTTGGTGG	3780
Db	3721	TGTGCGACGAAAGTTTCCGAAATCGCGGTTTTTTATTTTCCGCTTTTCACTTTGGTGG	3780
OY	3781	AATTTGAGAGGCGGACTTGGCATTTGGGCTTGGAGCGCTAGTCAACGGAACGTTGATTAACG	3840
Db	3781	AATTTGAGAGGCGGACTTGGCATTTGGGCTTGGAGCGCTAGTCAACGGAACGTTGATTAACG	3840
OY	3841	CGCGCCGCTTCCCGGCGTCAACGCTCTTGAATCGCGCTTTCACAGCACTATTCGTTGCTCT	3900
Db	3841	CGCGCCGCTTCCCGGCGTCAACGCTCTTGAATCGCGCTTTCACAGCACTATTCGTTGCTCT	3900
OY	3901	GCTTCTTGATCTACGTTGATTTAATAGTGTGAGCAATCGGGAATATTTTCTCTCCGC	3960
Db	3901	GCTTCTTGATCTACGTTGATTTAATAGTGTGAGCAATCGGGAATATTTTCTCTCCGC	3960
OY	3961	TGTGCGTTCGCGGATTTGGCGCTAATTTTCTTGATCTGCAACGGGCTCAGCTGTGTGATC	4020
Db	3961	TGTGCGTTCGCGGATTTGGCGCTAATTTTCTTGATCTGCAACGGGCTCAGCTGTGTGATC	4020
OY	4021	GGGGAATTACGCTGCGCAAAAGCTGACGGAAGCAAGCTCAAGCATCTCAGCGCCATTGCAT	4080
Db	4021	GGGGAATTACGCTGCGCAAAAGCTGACGGAAGCAAGCTCAAGCATCTCAGCGCCATTGCAT	4080
OY	4081	ACCTAGCCTCTGAGTATCTCGCGCTGCGCGGCTCTTGAGGCTCGGTTCAACGCTTGG	4140
Db	4081	ACCTAGCCTCTGAGTATCTCGCGCTGCGCGGCTCTTGAGGCTCGGTTCAACGCTTGG	4140
OY	4141	CCATCGCTTTGTGCTTGGAGCGGCTGTTCTTGCAATCTCAATTCGCGCGCTTCAAAAGTC	4200
Db	4141	CCATCGCTTTGTGCTTGGAGCGGCTGTTCTTGCAATCTCAATTCGCGCGCTTCAAAAGTC	4200
OY	4201	GAACTGCGCTTAATGCACTACCGGAACGATTAACCGAAAGTATTGTTAACCAGATCCGGC	4260
Db	4201	GAACTGCGCTTAATGCACTACCGGAACGATTAACCGAAAGTATTGTTAACCAGATCCGGC	4260
OY	4261	AGGTTTGTTCGACGCTGCGCAGATTAATTCGCTTGGTGCAGAAATCATATGTACCGGAAC	4320
Db	4261	AGGTTTGTTCGACGCTGCGCAGATTAATTCGCTTGGTGCAGAAATCATATGTACCGGAAC	4320
OY	4321	GATCTTCATGACGAGATTCGGGTTGCAAAACAAAGTCTGACGCTTCGGAGAGGATTCGC	4380

Best Local Similarity 100.0%; Pred. No. 0;
Matches 7142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGCGTAAAGACACAGACAGTCTCCGTAGACCATTAAGAGCTTTTAAAGACGCCAACGCA 60
Db 1 CGCGTAAAGACACAGACAGTCTCCGTAGACCATTAAGAGCTTTTAAAGACGCCAACGCA 60
QY 61 TAGACGCGGCTTTTCTTAAAGCTGTAGACGCTTGTAGCTTATTCCTTGTAGCGTAGAT 120
Db 61 TAGACGCGGCTTTTCTTAAAGCTGTAGACGCTTGTAGCTTATTCCTTGTAGCGTAGAT 120
QY 121 TGGATCGATATACAAAAGTATATCTCGCACTAACAGAGCGATCGACTCTCTTAC 180
Db 121 TGGATCGATATACAAAAGTATATCTCGCACTAACAGAGCGATCGACTCTCTTAC 180
QY 181 TAGTCCGCGAACCTTACTGCTTAAGAAATTTAGTGGCGGTTGTCAATCCATCGATAC 240
Db 181 TAGTCCGCGAACCTTACTGCTTAAGAAATTTAGTGGCGGTTGTCAATCCATCGATAC 240
QY 241 GTTTCGCGGCTGTCTTCCACACATCTATTTTCGCGAGAAATTCGCGTAGATGTC 300
Db 241 GTTTCGCGGCTGTCTTCCACACATCTATTTTCGCGAGAAATTCGCGTAGATGTC 300
QY 301 AGCCAGCAAAAGTCTGCGATTTGATCGCGCAATACAGCGGCGAGTGGCGCATCTAT 360
Db 301 AGCCAGCAAAAGTCTGCGATTTGATCGCGCAATACAGCGGCGAGTGGCGCATCTAT 360
QY 361 CGCCGAGCGTCACCAATTTCCGACAGAGGTTTTCTGCTGCAATATTTTTCTTTC 420
Db 361 CGCCGAGCGTCACCAATTTCCGACAGAGGTTTTCTGCTGCAATATTTTTCTTTC 420
QY 421 TGAATCGATATAGTGTGTTTTGTGTCTGCGATGATTCGCAACCGTTATTCG 480
Db 421 TGAATCGATATAGTGTGTTTTGTGTCTGCGATGATTCGCAACCGTTATTCG 480
QY 481 ATTGCGATTTGTCAAAATCTCAATATGATTTTAAAGACAAAGTAGGCTCA 540
Db 481 ATTGCGATTTGTCAAAATCTCAATATGATTTTAAAGACAAAGTAGGCTCA 540
QY 541 CATTTGTGCAAAATGATCTGCGCAAAACCCCAATGCTAAATGAGTGTGTCATAC 600
Db 541 CATTTGTGCAAAATGATCTGCGCAAAACCCCAATGCTAAATGAGTGTGTCATAC 600
QY 601 ATTAAGAGTGGCGAAGATGTCGAAGTGAAGAGGCTCCATCAAGGCACTTCAAG 660
Db 601 ATTAAGAGTGGCGAAGATGTCGAAGTGAAGAGGCTCCATCAAGGCACTTCAAG 660
QY 661 CTGCTGTTCTGAAGTGAAGAGAGTGCATCGAGGTAGCGGTCAAGGCTCGTCG 720
Db 661 CTGCTGTTCTGAAGTGAAGAGAGTGCATCGAGGTAGCGGTCAAGGCTCGTCG 720
QY 721 CTTAAGTGAACATCCGCGGAGTGCAGAAACGTAACCCGCACTTATGCGCTTCA 780
Db 721 CTTAAGTGAACATCCGCGGAGTGCAGAAACGTAACCCGCACTTATGCGCTTCA 780
QY 781 CGGAGTGTTCGCAATGAGATTTGTCCAAAGATTCGGAATCGACCGTCTTCACTCG 840
Db 781 CGGAGTGTTCGCAATGAGATTTGTCCAAAGATTCGGAATCGACCGTCTTCACTCG 840
QY 841 CTACTACAGCTCGACGCTATCTATATCGCGAGTTCAGAGTGCCTGCGAGAGCA 900
Db 841 CTACTACAGCTCGACGCTATCTATATCGCGAGTTCAGAGTGCCTGCGAGAGCA 900
QY 901 CATCACTCAATCGCTATTTTGGGACATTTGTGTCAGATTCATGACGCCAGAAATCT 960
Db 901 CATCACTCAATCGCTATTTTGGGACATTTGTGTCAGATTCATGACGCCAGAAATCT 960
QY 961 GGTAAAGCGTGTGAGAGCTATCCGATTAAGATCCCGAGAGTGGCGCGAGCATGCA 1020
Db 961 GGTAAAGCGTGTGAGAGCTATCCGATTAAGATCCCGAGAGTGGCGCGAGCATGCA 1020
QY 1021 AGGCAATGTCGAGTGGGCGATCATCGAACCGTGGGCTTGAAGACCGCAATTTGATCC 1080
Db 1021 AGGCAATGTCGAGTGGGCGATCATCGAACCGTGGGCTTGAAGACCGCAATTTGATCC 1080
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Db 1021 AGGCAATGTCGAGTGGGCGATCATCGAACCGTGGGCTTGAAGACCGCAATTTGATCC 1080
QY 1081 TTTGACGCTAGAGTGTCAATGTCGACAGGCAATGGGATTAATCACTGGCTCAAGTCG 1140
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QY 1141 CATGACCTGATCAATTAATCTGATGGGAGAGCGTTAAACGCCAGGACCTTGAACAAAT 1200
Db 1141 CATGACCTGATCAATTAATCTGATGGGAGAGCGTTAAACGCCAGGACCTTGAACAAAT 1200
QY 1201 GGAAGACATTTGTGCGAGAGGCTGTTCGTCGAATTTTCAAGGCGCAACTCTCG 1260
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QY 1261 ACCGAATATATTTGCAATTTAGTCCGCTGACAGCGTTCGAATTTCAATTAATCGGC 1320
Db 1261 ACCGAATATATTTGCAATTTAGTCCGCTGACAGCGTTCGAATTTCAATTAATCGGC 1320
QY 1321 GTCCGTGCAATTCGTCATGAGAGGACCGCTTCCGACGAACTGTGCTGATATAT 1380
Db 1321 GTCCGTGCAATTCGTCATGAGAGGACCGCTTCCGACGAACTGTGCTGATATAT 1380
QY 1381 CACATTCCTCTCAACTATGCGGCGCGCAAGACGATACCGTCAACATGTATGCACTGG 1440
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QY 1441 CGAGCATCTGGGAAAGGCGCTCCATCCGAGAGGCGGACACCCCATCGAATCTAGT 1500
Db 1441 CGAGCATCTGGGAAAGGCGCTCCATCCGAGAGGCGGACACCCCATCGAATCTAGT 1500
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Db 1561 TCAATCGGCTGATCTATGAAATAGCGTCCACTTGAAGCACTGCAAGAGGCAAG 1620
QY 1621 CTCAGTGTGCGGATTCAGGTCGCAAAACCGTTGGGCTTTCCTTCAATTAATGTCG 1680
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QY 1741 TCTTGGGATATTCATGCAATGCAAGAGTTTGGTCCAAATCTCGGCTCGATTTGAG 1800
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QY 1801 TGAACCTTTTCTGTGCGGAAAGCATGTTGAAGGCTCTTGAAGCTCGATTCGTTAT 1860
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QY 1861 CGAGTCCGAGATGTCAGCTTGTGCTGTCACAGACGAGAACCAACATGATTAAGTGC 1920
Db 1861 CGAGTCCGAGATGTCAGCTTGTGCTGTCACAGACGAGAACCAACATGATTAAGTGC 1920
QY 1921 GCCGCTTCTCAACTGATCTTGAAGTGAATCCGCGTCTCAAGACCTCTGACCG 1980
Db 1921 GCCGCTTCTCAACTGATCTTGAAGTGAATCCGCGTCTCAAGACCTCTGACCG 1980
QY 1981 CGGACAGCTTTTCTTCAACGATGTTGAATCTTGGCGTAACTTCACACATTCGCAAGA 2040
Db 1981 CGGACAGCTTTTCTTCAACGATGTTGAATCTTGGCGTAACTTCACACATTCGCAAGA 2040
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Db 2041 AACACCCGCGCAAGCTGGGATTTGGTGTGCTGATGAGCGTGTGATGTTGAC 2100
QY 2101 AAACCAACCGCTGCGACCATCGAAGCATTTGTTAGCTTGTGTTGTCATCCG 2160
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 11:30:31 ; Search time 1632 Seconds
(without alignments)
15949,401 Million cell updates/sec

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Perfect score: 7142
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7142	100.0	7142	9	US-09-927-616A-7
3	42	0.6	612	13	US-10-027-632-235765
4	42	0.6	612	13	US-10-027-632-235766
5	42	0.6	612	13	US-10-027-632-235767
6	42	0.6	612	13	US-10-027-632-235765
7	42	0.6	612	14	US-10-027-632-235765
8	42	0.6	612	14	US-10-027-632-235766
9	41.2	0.6	777	15	US-10-184-644-348
10	40.4	0.6	594	13	US-10-140-472-10
11	40.4	0.6	594	13	US-10-141-761-10
12	40.4	0.6	594	13	US-10-142-885-10
13	40.4	0.6	594	13	US-10-158-790-10
14	40.4	0.6	594	13	US-10-137-871-10
15	40.4	0.6	594	13	US-10-137-871-10

16	40.4	0.6	594	13	US-10-140-805-10	Sequence 10, Appl
17	40.4	0.6	594	13	US-10-140-864-10	Sequence 10, Appl
18	40.4	0.6	594	13	US-10-140-923-10	Sequence 10, Appl
19	40.4	0.6	594	13	US-10-141-756-10	Sequence 10, Appl
20	40.4	0.6	594	13	US-10-141-759-10	Sequence 10, Appl
21	40.4	0.6	594	15	US-10-123-155-10	Sequence 10, Appl
22	40.4	0.6	594	16	US-10-146-731-10	Sequence 10, Appl
23	39.6	0.6	1184	13	US-10-140-472-412	Sequence 412, App
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25	39.6	0.6	1184	13	US-10-142-885-412	Sequence 412, App
26	39.6	0.6	1184	13	US-10-158-790-412	Sequence 412, App
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29	39.6	0.6	1184	13	US-10-140-864-412	Sequence 412, App
30	39.6	0.6	1184	13	US-10-140-923-412	Sequence 412, App
31	39.6	0.6	1184	13	US-10-141-756-412	Sequence 412, App
32	39.6	0.6	1184	13	US-10-141-759-412	Sequence 412, App
33	39.6	0.6	1184	15	US-10-123-155-412	Sequence 412, App
34	39.6	0.6	1184	16	US-10-146-731-412	Sequence 412, App
35	39.6	0.6	99116	13	US-10-298-132-1	Sequence 1, Appl
36	39.2	0.5	818	13	US-10-027-632-169217	Sequence 169217, App
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38	39.2	0.5	915	13	US-10-140-472-294	Sequence 294, App
39	39.2	0.5	915	13	US-10-141-761-294	Sequence 294, App
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42	39.2	0.5	915	13	US-10-137-871-294	Sequence 294, App
43	39.2	0.5	915	13	US-10-140-805-294	Sequence 294, App
44	39.2	0.5	915	13	US-10-140-864-294	Sequence 294, App
45	39.2	0.5	915	13	US-10-140-923-294	Sequence 294, App

ALIGNMENTS

RESULT 1
US-09-927-616A-1
; Sequence 1, Application US/09927616A
; Patent No. US20020090354A1
; GENERAL INFORMATION:
; APPLICANT: Triplet, Eric W
; TITLE OF INVENTION: Biological Control of Crown Gall Disease
; FILE REFERENCE: 960296, 97273
; CURRENT APPLICATION NUMBER: US/09/927, 616A
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/224,929
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7142
; TYPE: DNA
; ORGANISM: Rhizobium leguminosarum bv. trifolii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (597)..(722)
; OTHER INFORMATION: tfixa coding sequence
; NAME/KEY: CDS
; LOCATION: (794)..(1912)
; OTHER INFORMATION: tfixb coding sequence
; NAME/KEY: CDS
; LOCATION: (2982)..(4229)
; OTHER INFORMATION: tfixd coding sequence
; NAME/KEY: CDS
; LOCATION: (4968)..(5741)
; OTHER INFORMATION: tfixf coding sequence
; NAME/KEY: CDS
; LOCATION: (5996)..(6778)
; OTHER INFORMATION: tfixg coding sequence
US-09-927-616A-1
Query Match 100.0%; Score 7142; DB 9; Length 7142;

Matches 62; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 512 TGCATTTTAAAGACAGATAGGCTCACATTTGTCAGCAATGACTGCGCAAAACC 571
DB 510 TACATTTTACAAATAGCAGCAAAATTCCTCAATTTTATCTATGACCTATTTCAAACC 451
QY 572 CAATGCTAAATGAGGTGTGTTGCATGATTAACAAGTTGCGAA 616
DB 450 CAACGATACCTAGAACTTAATTCATTTTACATATTTCAA 406

RESULT 14

US-08-362-577C-4/c
Sequence 4, Application US/08362577C
Patent No. 5807673

GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
FILING DATE: 27-MAR-1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: Clinical Isolate SA-77
US-08-362-577C-4

Query Match 0.5%; Score 36.2; DB 1; Length 2885;
Best Local Similarity 59.0%; Pred. No. 3.2;
Matches 62; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 512 TGCATTTTAAAGACAGATAGGCTCACATTTGTCAGCAATGACTGCGCAAAACC 571
DB 510 TACATTTTACAAATAGCAGCAAAATTCCTCAATTTTATCTATGACCTATTTCAAACC 451

QY 572 CAATGCTAAATGAGGTGTGTTGCATGATTAACAAGTTGCGAA 616
DB 450 CAACGATACCTAGAACTTAATTCATTTTACATATTTCAA 406

RESULT 15
US-08-920-828-4/c

Sequence 4, Application US/08920828
Patent No. 5853998

GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: Clinical Isolate SA-77
US-08-920-828-4

Query Match 0.5%; Score 36.2; DB 2; Length 2885;
Best Local Similarity 59.0%; Pred. No. 3.2;
Matches 62; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 512 TGCATTTTAAAGACAGATAGGCTCACATTTGTCAGCAATGACTGCGCAAAACC 571
DB 510 TACATTTTACAAATAGCAGCAAAATTCCTCAATTTTATCTATGACCTATTTCAAACC 451

QY 572 CAATGCTAAATGAGGTGTGTTGCATGATTAACAAGTTGCGAA 616
DB 450 CAACGATACCTAGAACTTAATTCATTTTACATATTTCAA 406

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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: Clinical Isolate SA-77
US-08-920-812-4

Query Match 0.5%; Score 36.2; DB 1; Length 2885;
Best Local Similarity 59.0%; Pred. No. 3.2;
Matches 62; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 512 TGCATTTTAAAGACAGATAGCTGCTACATTTGTGACGAAATGACTGCTGGCAAAACC 571
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QY 572 CAATGCTAATAGAGTGTGTCGATGATACAGAGTTGCGAA 616
DB 450 CAACGATACAGAACTTAATTCATTTTAAACATGATTCAAA 406

RESULT 12
US-08-920-827-4/c
Sequence 4, Application US/08920827
Patent No. 5770375
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: Clinical Isolate SA-77
US-08-920-827-4

Query Match 0.5%; Score 36.2; DB 1; Length 2885;
Best Local Similarity 59.0%; Pred. No. 3.2;
Matches 62; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 512 TGCATTTTAAAGACAGATAGCTGCTACATTTGTGACGAAATGACTGCTGGCAAAACC 571
DB 510 TACATTTTCAAAATAGCGCAAAATTTCTCAATTTTATCTATGACCTATTTCAAACC 451

QY 572 CAATGCTAATAGAGTGTGTCGATGATACAGAGTTGCGAA 616
DB 450 CAACGATACAGAACTTAATTCATTTTAAACATGATTCAAA 406

RESULT 13
US-08-921-177-4/c
Sequence 4, Application US/08921177
Patent No. 5798211
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: Clinical Isolate SA-77
US-08-921-177-4

Query Match 0.5%; Score 36.2; DB 1; Length 2885;
Best Local Similarity 59.0%; Pred. No. 3.2;

NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11544
LENGTH: 852
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11544

Query Match 0.5%; Score 37; DB 4; Length 852;
Best Local Similarity 48.0%; Pred. No. 0.8; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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QY 6674 ACGCCAGAGTCGACAGATCGCGAACCCTATGCGCAATTGCTGCGCAGCTAGAAAGTGC 6733
DB 188 CCAGCAGGAGTGGGCGGCGCGGCTGCTCCAGCGCAGAGCTGCGCGGAAACTCGATCC 247
QY 6734 TCCTGATGCTTCATCATCGCGCAACACTGGAAGCGGCTGGCATAGGAGCAGCGACC 6793
DB 248 GCGCTTTTCATCGCGCTCGGCTCGCTCAGCGCGCCAGACTCGCCAGCGCCGAGTACT 307
QY 6794 GCGCCATAGTCTGTGGAGCAAGCTGCGAGCTGCGGCTTGGC 6834
DB 308 GGGCGACAGGCGCATCGGCTGGCGCCGCGGCTGGGTAGCG 348

RESULT 9
US-09-252-991A-11665
Sequence 11665, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11665
LENGTH: 1608
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11665

Query Match 0.5%; Score 37; DB 4; Length 1608;
Best Local Similarity 48.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 6614 GACAAGCTAATCAGCTTGCAGTTCACGATGCGCGCCGAGCAGCAAGAGCGGCTGTC 6673
DB 1047 GACCATCGAGTTCCAGGCGGAGCGCCCGCCGAGCGGCTGTCGCAACTGCGGCTGCTGT 1106
QY 6674 ACGCCAGAGTCGACAGATCGCGAACCCTATGCGCAATTGCTGCGCAGCTAGAAAGTGC 6733
DB 1107 CCAGCAGGAGTGGGCGGCGCGGCTGCTCCAGCGCAGAGCTCGGCGGAAACTCGATCC 1166
QY 6734 TCCTGATGCTTCATCATCGCGCAACACTGGAAGCGGCTGGCATAGGAGCAGCGACC 6793
DB 1167 GCGCTTTTCATCGCGCTCGGCTCGCTCAGCGCGCAGAGCTCGCCAGCGCCGAGTACT 1226
QY 6794 GCGCCATAGTCTGTGGAGCAAGCTGCGAGCTGCGGCTTGGC 6834
DB 1227 GGGCGACAGGCGCATCGGCTGGCGCCGCGGCTGGGTAGCG 1267

RESULT 10
US-09-252-991A-11769/c

Sequence 11769, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11769
LENGTH: 1608
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11769

Query Match 0.5%; Score 37; DB 4; Length 1608;
Best Local Similarity 48.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 6614 GACAAGCTAATCAGCTTGCAGTTCACGATGCGCGCCGAGCAGCAAGAGCGGCTGTC 6673
DB 784 GACCATCGAGTTCCAGGCGGAGCGCCCGCCGAGCGGCTGTCGCAACTGCGGCTGCTGT 725
QY 6674 ACGCCAGAGTCGACAGATCGCGAACCCTATGCGCAATTGCTGCGCAGCTAGAAAGTGC 6733
DB 724 CCAGCAGGAGTGGGCGGCGCGGCTGCTCCAGCGCAGAGCTCGCGGAAACTCGATCC 665
QY 6734 TCCTGATGCTTCATCATCGCGCAACACTGGAAGCGGCTGGCATAGGAGCAGCGACC 6793
DB 664 GCGCTTTTCATCGCGCTCGGCTCGCTCAGCGCGCCAGACTCGCAGCGCCGAGTACT 605
QY 6794 GCGCCATAGTCTGTGGAGCAAGCTGCGAGCTGCGGCTTGGC 6834
DB 604 GGGCGACAGGCGCATCGGCTGGCGCCGCGGCTGGGTAGCG 564

RESULT 11
US-08-920-812-4/c
Sequence 4, Application US/08920812
Patent No. 5763188
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Lt-Hsien

Best Local Similarity 7.9%; Pred. No. 0.00039;
Matches 34; Conservative 211; Mismatches 185; Indels 0; Gaps 0;

```
OY 3765 TTTTCTACCTTGTGGAATGACGACCGACTTGCGCTTGAGCGCTCACTAC 3824
    |||||
DB 996 TTTTCTCTGCTTCCATACCGCTCAGAAATTAATCCGAGCTTGCGTCACTG 1055
    |||||
OY 3825 GAACGCTTGATAGCCCGCGCGCTTCCCGCGCTGACAGTGTATGCGCTTACAGC 3884
    |||||
DB 1056 GAGCTGCGAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1115
    |||||
OY 3885 ACGTATGCTGCTGCTGCTTCTGATGATGATGATGATGATGATGATGATG 3944
    |||||
DB 1116 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1175
    |||||
OY 3945 ATATTGCTCTCCGCTGCTGCTTGGCGGATGCGGCTACTTTCTGATGCGAGG 4004
    |||||
DB 1176 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1235
    |||||
OY 4005 CTGCACTGTGCTGCGGAGATATACGCTCGCGCAAGCTGAGGAGGAGCTACGCAT 4064
    |||||
DB 1236 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1295
    |||||
OY 4065 CTGACGCGCATGCACTACCTAGCTCTGAGATGATCTGCGCGCGCTTGTGGGC 4124
    |||||
DB 1296 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1355
    |||||
OY 4125 TCGGTTCAAGCGTGGCCATCGCTTGTGCTTGGAGCGCTGTCTGCAATCTGCATT 4184
    |||||
DB 1356 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1415
    |||||
OY 4185 CCGCGCGCTTC 4194
    |||||
DB 1416 TTTTTTTTTT 1425
    |||||
```

RESULT 2

US-09-372-422A-31/c
; Sequence 31, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barlieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1015
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (77)...(863)
US-09-372-422A-31

Query Match
Best Local Similarity 0.6%; Score 42.6; DB 4; Length 1015;
Matches 93; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

```
OY 6501 ATGACGACATTCGAGAGAGGATGATGATGATGATGATGATGATGATGATTC 6560
    |||||
DB 540 ATGACGAGCTTCAGAGAGGAGGAGGATGATGATGATGATGATGATGATGAT 481
    |||||
OY 6561 GCTGCTGTTGAGCGGCTATGCTGTCTGCGAAGAGAGCGCGGCTTCTGCAACG 6620
    |||||
DB 480 GCGGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
    |||||
OY 6621 TATACAGTTGCAATGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6677
    |||||
```

DB 420 AGCTGCGGAGCCAGTCAAGACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 364
|||||

RESULT 3

US-09-252-991A-13246
; Sequence 13246, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13246
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13246

Query Match
Best Local Similarity 0.5%; Score 39; DB 4; Length 1803;
Matches 84; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

```
OY 4034 CGCCAAAGCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4093
    |||||
DB 213 CGGTAAGACTTCAAGCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 272
    |||||
OY 4094 AGTATCTCTGCGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4153
    |||||
DB 273 AGTACCGCTGCTGCTGCGGCGGCTGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTG 332
    |||||
OY 4154 CTGGAGCGGCTGCTTCTTGCATCTCATCTCCGCGCT 4192
    |||||
DB 333 CGTGAGGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 371
    |||||
```

RESULT 4

US-09-252-991A-12713/c
; Sequence 12713, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12713
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12713

Query Match
Best Local Similarity 0.5%; Score 39; DB 4; Length 1878;
Matches 84; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

```
OY 4034 CGCCAAAGCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4093
    |||||
DB 1603 CGGTAAGACTTCAAGCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1544
    |||||
```


PS Claim 12; 56bp + Sequence Listing; 56bp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridized to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridization to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridized to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (1) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (1i) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 969 BP; 177 A; 54 C; 93 G; 645 T; 0 other;

Query Match 0.6%; Score 39.4; DB 24; Length 969;
Best Local Similarity 56.6%; Pred. No. 0.9; Mismatches 56; Indels 0; Gaps 0;
Matches 73; Conservative 0;

OY 392 TTTTCTGCGTCGACAAATTTTCTTCTTCGATGATCATAGTGTGTTTGTTCG 451
DB TTTTCTGCGTCGTCGTAATATTTTATTTTATTTTATTTTATTCGTTTATGAT 185
OY 432 TCTGACGATTTGCAACCGTTTGATTCGATTCGATTTTGCAGAAATCTCATATGAT 511
DB TTTATTCGATTTTATTCGTTTATTTAGTATTTTATTCGATTTTATTCGTTTAT 245
OY 512 TGCATTTT 520
DB 246 AGTATTTT 254

RESULT 11
ABQ39491/C
ID ABQ39491 standard; DNA; 969 BP.
XX
AC ABQ39491;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 26082.

XX
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP10074.

XX 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Gietig D;

XX WPI; 2002-371829/40.

XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
XX for diagnosis and prognosis, comprises selective hybridization of
XX amplicons from chemically treated DNA -
PS Claim 12; 56bp + Sequence Listing; 56bp; German.

XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridized to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridization to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridized to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (1) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (1i) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 969 BP; 645 A; 93 C; 54 G; 177 T; 0 other;

Query Match 0.6%; Score 39.4; DB 24; Length 969;
Best Local Similarity 56.6%; Pred. No. 0.9; Mismatches 56; Indels 0; Gaps 0;
Matches 73; Conservative 0;

OY 392 TTTTCTGCGTCGACAAATTTTCTTCTTCGATGATCATAGTGTGTTTGTTCG 451
DB 844 TTTATTCGATTTTATTCGTTTATTTAGTATTTTATTCGATTTTATTCGTTTAT 785
OY 452 TCTGACGATTTGCAACCGTTTGATTCGATTCGATTTTGCAGAAATCTCATATGAT 511
DB 784 TTTATTCGATTTTATTCGTTTATTTAGTATTTTATTCGATTTTATTCGTTTAT 725

OY 512 TGCATTTT 520
DB 724 AGTATTTT 716

RESULT 12
ABQ27378
ID ABQ27378 standard; DNA; 612 BP.
XX
AC ABQ27378;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 13969.

XX
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP10074.

XX 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.

PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 26-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 39.8; DB 21; Length 1313;
 Best Local Similarity 51.4%; Pred. No. 0.84;
 Matches 92; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 2520 AATCGTACCTTCAGTCTCTCCCTCGGATATACCTTTCACACGCCGCTTCTCAGCGTTGCC 2579
 DB 703 AATCTCACTCTAATTCCTCTCTGCGCGCTTCATCTGCACTTCTCTCGCGTTGAG 762
 QY 2580 ACCCTTGTGTCACATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 2639
 DB 763 ATCTGCACTTTCACATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 822
 QY 2640 TATCGTTACATTCGTCATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 2698
 DB 823 GATTCGCGTTCGTTGCTTAACTTATGATCTGGAATTCATGATCTCGAATGAGACGCT 881

RESULT 8
 ABQ42292
 ID ABQ42292 standard; DNA; 535 BP.
 AC ABQ42292;
 XX 12-JUL-2002 (first entry)
 DT
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28883.
 XX
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 XX SNP; cell differentiation; ds.
 XX
 XX Homo sapiens.
 OS
 PN MO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP10074.
 XX
 PR 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EP1G-) EPIGENOMICS AG.
 XX
 PI Oler A, Piepenbrock C, Berlin K, Guertig D;
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the

CC and therapy of solid tumours and cancer. The present sequence
CC represents one the 87 DNA sequences or its complement.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 12870 BP; 3344 A; 234 C; 3138 G; 6154 T; 0 other;

Query Match 0.6%; Score 42; DB 24; Length 12870;

Best Local Similarity 55.5%; Pred. No. 0.89; Indels 0; Gaps 0;

Matches 81; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

DB 389 AGGTTTCTCGTCGATTAATTTTCTTCCATGATCATTAGTGTGTTTGT 448

DB 5107 AGTTTCTGATTTTAAAGTATTTTGTGTAGTAATGTAATTTTATTTT 5166

DB 449 TGCCTGACGATTTGACACCGTTGATTCGATTCGATTCGATTCGATTC 508

DB 5167 TGTATTGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5226

DB 509 GATGCAATTTTAAAGCAAGATA 534

DB 5227 GGGTTGTTTAAATTTGTAAGTA 5252

RESULT 7

AAC47171 AAC47171 standard; DNA; 1313 BP.

AC AAC47171;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 52820.

XX Hybridisation assay; genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

XX metabolic pathway; promoter; termination sequence; BS.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 23-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0127462.

PR 01-APR-1999; 99US-0128234.

PR 06-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132485.

PR 05-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

QY 4036 CCAAGCTGAGGAGCAAGCTCAGGACATCTCAGGCCATTGCACTACCTAGCCTTGAG 4095
Db 9517 SSSDCTBYSSDRGSRSDTCTCYSCSDRSYTTTADACTTDAATBTCTTSDNCNSTRS 9458
QY 4096 TGATCTCGCGCTGCGCGCGCTTGGCTCGTTCAAGCGTGGCCATCGCTTGCT 4155
Db 9457 RCYNTSTYSCSRBTBSRNTCCCTBTSTRGNCYDAVDANSTRYAYYDACYSYDASTT 9398
QY 4156 TGGACCCGCTGTTCTGCATCTCCATTCCCGCGTTCAAGTGAAGTGCCTTAATG 4215
Db 9397 BYSYCTBYSTNSTDYASRSYCTCYTCDYSTCTYCTACAKCTBQNSTSRASRTTMTT 9338
QY 4216 CACTACCGA 4224
Db 9337 YRCYCTSR 9329

RESULT 5
ABL70230
ID ABL70230 standard; DNA; 12870 BP.

XX ABL70230;

DT 01-JUN-2002 (first entry)

DE Chemically treated cell signalling DNA sequence complementary to#60.

XX Cell signalling; cytosine methylation; cell signalling disease;

KW cancer; tumour; cytostatic; ds.

XX Unidentified.

OS WO200202807-A2.

XX 10-JAN-2002.

PD 29-JUN-2001; 2001WO-EP07471.

XX 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIG-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K;

PI WPI; 2002-154758/20.

DR Nucleic acid, useful for diagnosis and therapy of diseases associated

XX with cell signalling e.g. cancer, comprises chemically modified genomic

PT sequences of genes associated with cell signalling -

PS Claim 1; SEQ ID NO 120; 24pp+sequence listing; English.

XX The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signalling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell
CC signalling, as well as oligonucleotides and/or PNA-oligomers for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.

XX Sequence 12870 BP; 3344 A; 234 C; 3138 G; 6154 T; 0 other;

Query Match 0.6%; Score 42; DB 24; Length 12870;
Best Local Similarity 55.5%; Pred. No. 0.89;
Matches 81; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 389 AGGTTTCTCGCTCAGTAATTTTTTTCTTCTGATGATCATTAGTGTGTTTTTGT 448

Db 5107 AGTTTCTTTTAAAGTATTTTGTGTGATGATGATGATGATGATGATGATGATGAT 5166

QY 449 TGCTCTGACGATTTTGAACCGTTGATTTGATTTGCGTATTTGCAAAATACGCAAT 508

Db 5167 TGTATTAGGATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 5226

QY 509 GATTCATTTTAAAGACAAGATA 534

Db 5227 GGGTTGTTTTTAAATTGTAAGTA 5252

RESULT 6
ABK3984
ID ABK3984 standard; DNA; 12870 BP.

XX ABK3984;

DT 21-MAY-2002 (first entry)

DE Human chemically pretreated gene sequence #33 strand 2.

XX Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;

KW cytosine; ALDH6; CYP11A; CYP11B; CYP2A3; DYPD; EPHX2; OCLN; TXNRD1;

KW UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.

XX Homo sapiens.

OS WO200202806-A2.

XX 10-JAN-2002.

PD 29-JUN-2001; 2001WO-EP07470.

XX 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIG-) EPIGENOMICS AG.

PA Olek A, Piepenbrock C, Berlin K;

PI WPI; 2002-154757/20.

DR New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers,

XX useful for detecting cytosine methylation state of genes associated

PT with pharmacogenomics and for therapy of diseases e.g. cancer -

PS Claim 1; SEQ ID NO 66; 24pp; English.

XX The invention relates to a nucleic acid comprising a sequence at
CC least 18 bases in length of a segment of the chemically pretreated DNA
CC of genes associated with pharmacogenomics according to one of the
CC sequences of the genes ALDH6 (NM_000693), CYP11A (NM_000781), CYP11B1
CC (NM_000497), CYP2A3 (NM_000776 and NM_017460), DYPD (NM_000110), EPHX2
CC (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360),
CC MRP (NM_004996, NM_019900, NM_019901, NM_019902, NM_019862, NM_019898,
CC NM_019859) and their complementary sequences, or a sequence (SI) chosen
CC from 87 sequences and their complements. The chemical pretreatment
CC is bisulphite treatment to convert cytosines (but not methyl-cytosines)
CC into uracils. Also included are an oligomer (II) in particular an
CC oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in
CC each case at least one base sequence having a length of 9 nucleotides
CC which hybridises to or is identical to a chemically pretreated DNA of
CC genes associated with pharmacogenomics and their complements, arranged in
CC an array for analysing diseases associated with the methylation state
CC (CpG) and/or detecting SNPs (single nucleotide polymorphisms).
CC The set of 87 nucleic acids and their complements is useful for diagnosis

XX Disclosure; Page 48-50; 54pp; English.

CC The invention relates to novel transgenic organisms useful in the
CC production of functional food and drink products for the treatment
CC or prevention of obesity via the regulation of lipid metabolism. The
CC organisms comprise a polynucleotide encoding a growth hormone fragment
CC capable of stimulating the activity of hormone-sensitive lipase (the key
CC enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key
CC enzyme in lipogenesis). The growth hormone fragment preferably contains
CC at least the disulphide-bonded loop of a mammalian growth hormone (but is
CC not the full-length growth hormone) and is optionally linked to an
CC epitope tag or heterologous fusion protein partner. The transgenic
CC organism may be a microorganism used to produce a fermented product
CC (e.g., yeast), or an edible plant or animal or cell thereof. Food or
CC drink made using methods of the invention are used to modify fat/lean
CC ratio, lipid metabolism or food use in a mammal. In particular, the food
CC or drink products may be used to treat or prevent obesity, particularly
CC in humans, and may also be used to improve the fat/lean ration of
CC livestock raised for meat production. In the exemplification of the
CC invention, the human growth hormone (hGH) fragment analogue AOD9604 was
CC expressed in yeast, optionally fused to the FLAG epitope (AAB73625).
CC The present sequence is described as a DNA sequence from yeast in
CC the sequence listing, but is not further referred to in the
CC specification.

CC Sequence 4590 BP; 661 A; 384 C; 127 G; 522 T; 2896 other;

XX SQ
XX Query Match 0.6%; Score 43.2; DB 22; Length 4590;
XX Best Local Similarity 9.0%; Pred. No. 0.18; Mismatches 212; Indels 5; Gaps 1;
XX Matches 50; Conservative 288; Mismatches 212; Indels 5; Gaps 1;

QY 39 AGCTTTAGAGCAGCAAGCATACAGCGCTTTTAAAGTCTGACAGCTTGCG 98
DB 4376 AVSYTTSYRANVHHVNHCHADMGTDYACSHYHMASYKGRSHMGSHNH 4317
QY 99 TTATTCCTTGAGCGTACGATGATGATGATGATGATGATGATGATGATGAT 158
DB 4316 NSRHHMSDDSSRHHMSRHHMSRHHMSRHHMSRHHMSRHHMSRHHMSRHHMS 4257
QY 159 GAGCGGATCCGACCTCTCTACTAGTCCGCAAGCTTGATGAAATATGATGCG 218
DB 4256 NTKYNSKACKSSWMSWMSWMSWMSWMSWMSWMSWMSWMSWMSWMSWMSWMSWMS 4197
QY 219 GGTGTGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278
DB 4196 SRHHNHSTBTSRYBGATKASRHHNHSTBTSRYBGATKASRHHNHSTBTSRYBGAT 4137
QY 279 CGGCAAAATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 338
DB 4136 KAGSRHHNHSTB-TSRVGYATKASRHHNHSTBTSRYBGATKASRHHNHSTBTSRYBGAT 4082
QY 339 GGGCGGATCCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 398
DB 4081 RRYHHNHVHMRMMKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 4022
QY 399 GGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 458
DB 4021 NHTDDDDKGTNTTTHKKDKGADKDKDKDKDKDKDKDKDKDKDKDKDKDKDKDKDKDK 3962
QY 459 GTATTTGCAACGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 518
DB 3961 CHVTGANDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHND 3902
QY 519 TTTAAAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 578
DB 3901 HDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHNDHND 3842
QY 579 TAAATGAGGTGTGT 593
DB 3841 KAGHMSRHHNHKDSVK 3827

RESULT 4
AAA10594/C
ID AAA10594 standard; DNA; 10732 BP.

XX AAA10594;

XX 29-JUN-2000 (first entry)

DE Gene encoding a subunit of cellulose synthase.

KM Cellulose synthase; cellulose production; increase yield; ds.

XX Vigna angularis.

PN JP2000060568-A.

XX 29-FEB-2000.

PF 26-AUG-1998; 98JP-0239998.

PR 26-AUG-1998; 98JP-0239998.

PA (MIZU/) MIZUNO K.

PA (OJIP) OJI PAPER CO.

DR WPI; 2000-342371/30.

DR P-PSDB; AAY65179.

PT A gene encoding a cellulose synthetic equipment - for the improvement
PT in the amount of cellulose synthesised in a plant body

XX Claim 2; Page 14-21; 32pp; Japanese.

CC This sequence represents a gene encoding a subunit of the cellulose
CC synthase complex of Vigna angularis. The invention relates to subunits of
CC cellulose synthetic equipment, that can be used to increase the amount of
CC cellulose synthesised by a plant. The proteins and genes encoding them
CC can also be used to improve the properties of the cellulose being
CC produced by a plant.

SO Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;

XX Query Match 0.6%; Score 43; DB 21; Length 10732;
XX Best Local Similarity 14.8%; Pred. No. 0.38;
XX Matches 90; Conservative 249; Mismatches 261; Indels 9; Gaps 2;

QY 3618 GTCTTCTACTTGGAAAGCTGATCTGTCGGAATGCGGCGAGGCTTTCTGCGTCTTT 3677
DB 9930 STTNTSTCRCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 9871
QY 3678 ATCAACATGCTGGAATGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3737
DB 9870 BYRCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 9811
QY 3738 CCGCAATGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3797
DB 9810 DNSTNCYDASRBTSTSTNCYACRYBYDARCRDSTYSRG-----YDANSTRYS 9758
QY 3798 GCGATTTGGCTTGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3857
DB 9757 RYSSITSSDSTYSRACSTTBTBCTYUADYACUADYANCSYSTTBYCSRRCCT 9698
QY 3858 CTGACAGTCTTGTATGCGCGGTTTACACACAGATGATGATGATGATGATGATGATGATG 3917
DB 9697 YDAYSCTRYDARCTDAYSSTNSCTYDABTTRISITTSYSSNCTDATTSTBTSTST 9638
QY 3918 GATTAATAGTGTGAGCAATGCGGACATATTTGCTCCGCTGCTGCTGCGGATG 3977
DB 9637 BTTRCAKCTBDBSTSTANKSTSTYTRCTBYSRGRGYSRGRSRSRYSCTSDSTC 9578
QY 3978 GCGCTACTTTTCTGATCTGCAAGGCT--GCACTTGTGTTGCGGATATACGCTTG 4035
DB 9577 YSTTSTTAAVSCCTTGRGYSDASRSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 9518

QY 6082 GTCAACCCGATTTGCTGCGGATCGAAGCCTCT---GGCTGCTGAAGC 6138
 DB 9541 ASAAGYSASASYSYTHRSCTYSAASTRPAASRAASGASHANGSKSYSYGRSRC 9600
 QY 6139 TCCCTCCGTTGCGCAGCGGTTTCGATGAGCGCGCGGAGACATTAATGTTATGCA 6198
 DB 9601 XSYSRVAGYASASASNTMTASHVAGMTGYSAVAVASVAGYSAATHHGNRRSRA 9660
 QY 6199 GGGTACGTTGTTCCACCGCCCTTGTCGAGAGAGGCTTTCCGCAATTTGCAATGAT 6258
 DB 9661 ASRYSAAVAATHRGASNSRSRGTHRYGTHRSRTTHRGCGGYSGRVARASHSRGNTHR 9720
 QY 6259 GTTGGCGGACGTGACGATGCCACCGCTCGTTCAACCTCCGAAATCGATGTTGGG 6318
 DB 9721 THRGRTHRRKRVAAASMTGMTSRASHSASRSYSRTSASMTTHRCYSRASHYSGY 9780
 QY 6319 CGATTGTTGCGGCTTAACCTGATGAGGTCACACGTAATAGACATCGACACAG 6378
 DB 9781 THRVARGYTRGNVAVAVYSTRGNASNHSAVATHRHYSYGYRASHASASVVAALARG 9840
 QY 6379 CCCATGACATATTGTTCCCGGTCAGATTCCTGCTGCTGATGATGAGAGAGTGC 6438
 DB 9841 HSAASNSHSHASHASHS---RSRAGGYRVAHSASTRGNASNRNGCYSHSCYS 9895
 QY 6439 TGGGCTGTCAGGCGGATATGCAATTGGCCAGGCTTGCTGCAATGCCACCTCA 6498
 DB 9896 SRCYSSRASRSRVAAASNSRPAAGYASNAASRSRARGBRGNGASRSYSGY 9955
 QY 6499 CGATGACGACATTTGCGAGAGAGGTGCGATTGCTGCTGACCAAGAGCGCATCAAGT 6558
 DB 9956 SGVAGARBAVAALASTYRASRSRSGYSGYARAGSHRTYRYSANGYMTTRTHRG 10015
 QY 6559 TCGCTGCTGCTTGAACGCTATGCTGTCTGGAAGCAACGCGGCTTCTGACAA 6618
 DB 10016 YTYRMTVARGVAGHNTRYSTRSRSGRYSVAGHHSVACSTYRASRGYSTRASTY 10075
 QY 6619 GCTATTCAGTTCGAGTTACAGATCGCGCGAGAGGAGAAAGGCGGCTGACAGCC 6678
 DB 10076 RGYASNNHAAAGYTHRTHRAAASRTMASHCTSHSRGNASVARSMTARKASAAVSYSG 10135
 QY 6679 AGAGTCGAACGATGCGGACCGCTATGCGCAATGCTGCGCAGTGAAGTGCCTCTG 6738
 DB 10136 NHASTRASGTHRARSRASGYGASNGTHRHSAVAGSARGRSRRARGASNSRRGNA 10195
 QY 6739 GATGCTCATCATCGGCAAAACATGGAAGACCGCTGCAATAGGACGACCGCGCC 6798
 DB 10196 THRTSRSCYSGYHSAASNGYGYTYRTYRASNGYSGHTHRSYASYSRAAGSRGY 10255
 QY 6799 ATAAGTCGAGGACGAGAGCTGCGGCTGCGGCTGCGAGCTTAAGTTACGACCAAGAGG 6858
 DB 10256 SGVAARAGISGSRPAATHRASRAGSRMTASNGNGSGYSTHRRASPARGGSNRHVS 10315
 QY 6859 GAGACATATGAGACCTTCGTCAGGCGCTGCTGCTGCTTATCCACGAAAAAGATGC 6918
 DB 10316 GSRASNGNGGNSNGYASNSNGYASASNSRASAASGNSHTHGAAGYSAALHSAHSNTSV 10375
 QY 6919 AAC 6921
 DB 10376 AHS 10378

KW modulation; lipolysis stimulation; hormone-sensitive lipase stimulation;
 KW lipogenesis inhibition; acetyl CoA carboxylase inhibition; obesity;
 KW functional food; transgenic yeast; fat/lean ratio; food use; ds.
 OS Saccharomyces cerevisiae.
 Key Location/Qualifiers
 FT 10 misc_feature
 FT /tag= a
 FT /note= "Represented as * in the specification"
 FT 3617 misc_feature
 FT /tag= b
 FT /note= "Represented as * in the specification"
 FT 3649 misc_feature
 FT /tag= c
 FT /note= "Represented as * in the specification"
 FT 3679 misc_feature
 FT /tag= d
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 FT 3819 misc_feature
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 FT 4361 misc_feature
 FT /tag= q
 FT /note= "Represented as * in the specification"
 PN WO20013977-A1.
 XX 17-MAY-2001.
 XX 06-NOV-2000; 2000WO-AU01362.
 XX 05-NOV-1999; 99AU-0003875.
 XX (META-) METABOLIC PHARM LTD.
 XX Belyea CI, Ng FM, Vaughan P;
 XX WPI: 2001-328876/34.
 DR New organisms containing nucleic acid encoding a growth hormone
 PT fragment which modulates lipid metabolism are useful to produce dietary
 PT aids for obesity and in the meat production industry

QY 5881 GCGTCCCAAGCAGAGCGAGCCCTTGAAGTGCAGAAATGTTCCCGGGGGGAG 5940
DB 5881 GCGTCCCAAGCAGAGCGAGCCCTTGAAGTGCAGAAATGTTCCCGGGGGGAG 5940
QY 5941 GGTGAAGGTAAACCGCGCTTGTGTGCTAATGAATCCAGGTGGGTCATGA 6000
DB 5941 GGTGAAGGTAAACCGCGCTTGTGTGCTAATGAATCCAGGTGGGTCATGA 6000
QY 6001 TGATGAGATTTGCTGACAGGTGGCGAGCAAGCTGTCAGCGCGCGCGAGTGT 6060
DB 6001 TGATGAGATTTGCTGACAGGTGGCGAGCAAGCTGTCAGCGCGCGCGAGTGT 6060
QY 6061 GATGCGGAGGCGCGCGCTGTGATCAACCGCTCAATTCCTCTGCGCATTCG 6120
DB 6061 GATGCGGAGGCGCGCGCTGTGATCAACCGCTCAATTCCTCTGCGCATTCG 6120
QY 6121 CTCTGCGCTGCTGAGAGCTCTTCCGTTGTGCGGACCGGTTTCGATGAGCGCGCGG 6180
DB 6121 CTCTGCGCTGCTGAGAGCTCTTCCGTTGTGCGGACCGGTTTCGATGAGCGCGG 6180
QY 6181 GACATTAATGTTTATGAGAGGTGATGTTGTTCAACCGAGCCCTTGTGAGAGCTTT 6240
DB 6181 GACATTAATGTTTATGAGAGGTGATGTTGTTCAACCGAGCCCTTGTGAGAGCTTT 6240
QY 6241 TCCGCAATTTGGAATGATGTTGCGGCGACTGACAGATCCACCGCTCTTCAACCTCC 6300
DB 6241 TCCGCAATTTGGAATGATGTTGCGGCGACTGACAGATCCACCGCTCTTCAACCTCC 6300
QY 6301 CGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6360
DB 6301 CGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6360
QY 6361 AGGACATGCGCAGCAGAGCCCATGGAACATTTGTTGCGGATGAGCTGTCGAGGTT 6420
DB 6361 AGGACATGCGCAGCAGAGCCCATGGAACATTTGTTGCGGATGAGCTGTCGAGGTT 6420
QY 6421 GATGATTTGGAGGTGCTGCGCTGTGACGCGCGATTCGATTTGCGCGCTGTTG 6480
DB 6421 GATGATTTGGAGGTGCTGCGCTGTGACGCGCGATTCGATTTGCGCGCTGTTG 6480
QY 6481 GCTGAATGCCAGCTCTACGATGACGATTCGCGAGAGGCTCGGATTTAGCTCTGTAC 6540
DB 6481 GCTGAATGCCAGCTCTACGATGACGATTCGCGAGAGGCTCGGATTTAGCTCTGTAC 6540
QY 6541 CATGAGAGCGCATCAAGTTGCGCTGCTGATGACGCTGATGATGATGATGATGATGAT 6600
DB 6541 CATGAGAGCGCATCAAGTTGCGCTGCTGATGACGCTGATGATGATGATGATGATGAT 6600
QY 6601 CGGCGGCTTCTGCAAGCTAATCACTTTCGAGTTGACGATGCGCGCGAGCGGAA 6660
DB 6601 CGGCGGCTTCTGCAAGCTAATCACTTTCGAGTTGACGATGCGCGCGAGCGGAA 6660
QY 6661 AGAGCGGCTGTCAGCGCAGAGTGCAGAGATGCGGAACTGATGAGGATTTGCTGCGC 6720
DB 6661 AGAGCGGCTGTCAGCGCAGAGTGCAGAGATGCGGAACTGATGAGGATTTGCTGCGC 6720
QY 6721 CACTGAGAGTGCCTCTGATGCTCATCATCGGCAACACATGGAAGCGCTGCGGATA 6780
DB 6721 CACTGAGAGTGCCTCTGATGCTCATCATCGGCAACACATGGAAGCGCTGCGGATA 6780
QY 6781 GTAGGACGAGCAGCGCGCATTAAGTGTGGAAGAGCTGCGGATGCGGATGCGAGGTTA 6840
DB 6781 GTAGGACGAGCAGCGCGCATTAAGTGTGGAAGAGCTGCGGATGCGGATGCGAGGTTA 6840
QY 6841 AGTTGAGCAGCAGAGGAGGAGACATTAAGAGCTTCTTCAAGCGCTTCTGCGCTTTA 6900
DB 6841 AGTTGAGCAGCAGAGGAGGAGACATTAAGAGCTTCTTCAAGCGCTTCTGCGCTTTA 6900
QY 6901 TCCAGGAAAAACAGTGAATCTCTGAGAGAGCTGCAAAAAGTCCGAAAGGCTCTGCGC 6960
DB 6901 TCCAGGAAAAACAGTGAATCTCTGAGAGAGCTGCAAAAAGTCCGAAAGGCTCTGCGC 6960
QY 6961 TGTGTGACGCGCTGCTGATCCGGAATATTTCTTCTGCTTGAAGAGAGCGATTCAGC 7020

DB 6961 TGTGTGACGCGCTGCTGATCCGGAATATTTCTTCTGCTTGAAGAGAGCGATTCAGC 7020
QY 7021 TCTACTATGCGGAGCGGCGCATCTATTCATGAGTTCAGGCTGCGGAGTGCACAC 7080
DB 7021 TCTACTATGCGGAGCGGCGCATCTATTCATGAGTTCAGGCTGCGGAGTGCACAC 7080
QY 7081 GGAACCATGTAAGTACCTGTTCTGACAGCAGCGTACCTTACATCAAGATCAGAA 7140
DB 7081 GGAACCATGTAAGTACCTGTTCTGACAGCAGCGTACCTTACATCAAGATCAGAA 7140
QY 7141 CG 7142
DB 7141 CG 7142
RESULT 2
AAA10594
ID AAA10594 standard; DNA; 10732 BP.
XX
AC AAA10594;
XX
DT 29-JUN-2000 (first entry)
XX
DE Gene encoding a subunit of cellulose synthase.
XX
KM Cellulose synthase; cellulose production; increase yield; ds.
XX
OS Vigna angularis.
XX
XN JP2000060568-A.
XX
PD 29-FEB-2000.
XX
PF 26-AUG-1998; 98UP-0239998.
XX
PR 26-AUG-1998; 98UP-0239998.
XX
PA (MIZU) MIZUNO K.
XX
PA (OJIP) OJI PAPER CO.
XX
DR WPI; 2000-342371/30.
XX
DR P-PSDB; AAY85179.
XX
PT A gene encoding a cellulose synthetic equipment - for the improvement
XX
PT in the amount of cellulose synthesised in a plant body
XX
PS Claim 2; Page 14-21; 32pp; Japanese.
XX
CC This sequence represents a gene encoding a subunit of the cellulose
XX
CC synthase complex of Vigna angularis. The invention relates to subunits of
XX
CC cellulose synthetic equipment, that can be used to increase the amount of
XX
CC cellulose synthesised by a plant. The proteins and genes encoding them
XX
CC can also be used to improve the properties of the cellulose being
XX
XX produced by a plant.
XX
SQ Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;
Query Match 0.7%; Score 47; DB 21; Length 10732;
Best Local Similarity 12.4%; Pred. No. 0.021;
Matches 127; Conservative 402; Mismatches 486; Indels 8; Gaps 2;
QY 5902 AGGCCCTTGAAGTGCAGAAATGTTGCCGCGGCGGAGCTGGAAGCTGAACGCGGCC 5961
DB 5902 AGGCCCTTGAAGTGCAGAAATGTTGCCGCGGCGGAGCTGGAAGCTGAACGCGGCC 5961
QY 9361 ARGASSRHGARGARGSRYSRTHRASNSRVASRSRVASTHRSRGTHRTYRSASNT 9420
DB 9361 ARGASSRHGARGARGSRYSRTHRASNSRVASRSRVASTHRSRGTHRTYRSASNT 9420
QY 5962 TTGTGTGCTACTAATGAATCCAGGTGGTCCCATGATGATGATTTGCTGACAG 6021
DB 5962 TTGTGTGCTACTAATGAATCCAGGTGGTCCCATGATGATGATTTGCTGACAG 6021
QY 9421 HRTHRGNTYSAVAAGGASNTSVAYSGRSANAGYASNSGNSRPARGVAMTHRAR 9480
DB 9421 HRTHRGNTYSAVAAGGASNTSVAYSGRSANAGYASNSGNSRPARGVAMTHRAR 9480
QY 6022 TGGCGGAGCAAGCATGTCAGCGCGCGCGGAGATGCTGTATTCGGAAGCGCGCGCTG 6081
DB 6022 TGGCGGAGCAAGCATGTCAGCGCGCGCGGAGATGCTGTATTCGGAAGCGCGCGCTG 6081
QY 9481 THRASRYSHSGSRGASHSYSGYHSRVASHSHSRASNYVAASRHSRHSRHAASRSR 9540
DB 9481 THRASRYSHSGSRGASHSYSGYHSRVASHSHSRASNYVAASRHSRHSRHAASRSR 9540

Db 3661 GCGTTTCTGCGTCTTTATCAACATGCTGCAATGCGGTTTCTTGCAATGATGGGT363 3720
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Qy 3841 GCGCGCCGTTTCCCGGCTGCAAGCTTGTATCGCGTTTACAGACGTAATTCGTTGCTCT 3900
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Db 3901 GCTTCTGATCTAGCGTGAATTAATAGTGTAGGAGCAATTTGCTCCGCG 3960
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QY	1501	GGTGTCCGGCAGATGATGTCGAGATACGAAAGCTCCGATATATCTCAATGTTCCGCA	1560
Dp	1501	GGTGTCCGGCAGATGATGTCGAGATACGAAAGCTCCGATATATCTCAATGTTCCGCA	1560
QY	1561	TCATCCGCTCGATGCTATCGAATAAGACGTCCACTTATGAAAGCACTGCAGAAGCAG	1620
Dp	1561	TCATCCGCTCGATGCTATCGAATAAGACGTCCACTTATGAAAGCACTGCAGAAGCAG	1620
QY	1621	CTCAGTGTGCCCCCATATCAGGTCAAAACCGTTCCGGCTTTGGTTTCATTATCATGTCCG	1680
Dp	1621	CTCAGTGTGCCCCCATATCAGGTCAAAACCGTTCCGGCTTTGGTTTCATTATCATGTCCG	1680
QY	1681	GTTCCAGCGAAGATATGTTTCGGTACCGCGAACCAGGAACTACCGTGTGATGCACTTTGA	1740
Dp	1681	GTTCCAGCGAAGATATGTTTCGGTACCGCGAACCAGGAACTACCGTGTGATGCACTTTGA	1740
QY	1741	TCCTGGGCAATACCATGCAACGAGGTTTTGGCTCCCAAAAATCCTCCGCTCGATTTCAG	1800
Dp	1741	TCCTGGGCAATACCATGCAACGAGGTTTTGGCTCCCAAAAATCCTCCGCTCGATTTCAG	1800
QY	1801	TGAAACCTTTTCTGTGCGCGAAGCATATGTTGAGCGCTCTTGACGCTCGATCCGTTTAT	1860
Dp	1801	TGAAACCTTTTCTGTGCGCGAAGCATATGTTGAGCGCTCTTGACGCTCGATCCGTTTAT	1860
QY	1861	CGAGTCGCGAGATGATGAGCTTTGTCTGTCCACAGACAGAGAAACCAACATGATGAACTGC	1920
Dp	1861	CGAGTCGCGAGATGATGAGCTTTGTCTGTCCACAGACAGAGAAACCAACATGATGAACTGC	1920
QY	1921	GCCCCCTTCTCCAACTGAACTCTTGAGATGGAATCCCGGCTCTCAAAAGCACTCTCGACCG	1980
Dp	1921	GCCCCCTTCTCCAACTGAACTCTTGAGATGGAATCCCGGCTCTCAAAAGCACTCTCGACCG	1980
QY	1981	CCGACAGCTTTTCTTCAACCGATGTTGAATCTTTGCGGTATCATTCACCCATTCGCACAGA	2040
Dp	1981	CCGACAGCTTTTCTTCAACCGATGTTGAATCTTTGCGGTATCATTCACCCATTCGCACAGA	2040
QY	2041	ACACCCCCCGCCACAGCTCGGGAATTTGGCTGCTCTGTGCTGATGAGCGCTGATGTTGACC	2100
Dp	2041	ACACCCCCCGCCACAGCTCGGGAATTTGGCTGCTCTGTGCTGATGAGCGCTGATGTTGACC	2100
QY	2101	AAACCAACCGGCTCGACAGCTCGAAGCAATGTTGTAAGCTTTGTTGGTGCATCCG	2160
Dp	2101	AAACCAACCGGCTCGACAGCTCGAAGCAATGTTGTAAGCTTTGTTGGTGCATCCG	2160
QY	2161	CGTCGATCTCTCCGAGAAAGCGAGGATCCAGTTGTGGTGTGATTAAGGATGGGTGACG	2220
Dp	2161	CGTCGATCTCTCCGAGAAAGCGAGGATCCAGTTGTGGTGTGATTAAGGATGGGTGACG	2220
QY	2221	CACATGATCTCTGATTTCCGCGACAGAAATCTCAATTAATAGACATTCATTTGAATTTG	2280
Dp	2221	CACATGATCTCTGATTTCCGCGACAGAAATCTCAATTAATAGACATTCATTTGAATTTG	2280
QY	2281	GCAGGTTGGAAGATATCAAAAGCTATCCGCAACCGATGGAATCGAAGCGTATGAGAAACGCG	2340
Dp	2281	GCAGGTTGGAAGATATCAAAAGCTATCCGCAACCGATGGAATCGAAGCGTATGAGAAACGCG	2340
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Dp	2341	GCACCGCCACGCGATTTGTCAAAGCCGTCCTCCGAGCTGCGACGTGCACTATCTGACG	2400
QY	2401	GGCTCATATACAGGGCGCTGTTCAAAACCTTTCACACGCAACCACTGTGATTCACGAGG	2460
Dp	2401	GGCTCATATACAGGGCGCTGTTCAAAACCTTTCACACGCAACCACTGTGATTCACGAGG	2460
QY	2461	TCAGGAGATATCTTTGTTTGGGAAACCTCTATGCGCGAGAAACGCGCGGTCAATCGCTGAAA	2520
Dp	2461	TCAGGAGATATCTTTGTTTGGGAAACCTCTATGCGCGAGAAACGCGCGGTCAATCGCTGAAA	2520
QY	2521	ATCGGATTTGAGAGTCTCTCGCGATATAGCTTTGACAGAGCGCTTTCACAGCTTTGCCA	2580
Dp	2521	ATCGGATTTGAGAGTCTCTCGCGATATAGCTTTGACAGAGCGCTTTCACAGCTTTGCCA	2580
QY	2581	CCTTTGTGTCAATATGACAGATCGATTGGACAGATGAGCTCGTTGCGACCCGAGACTT	2640

Db	2581	CGTTTGTGTGCACATATGAGCAAGTCGATTTGGAGATGGCTGTGTCACACCGGAGTCT	2640
Oy	2641	ATCGTTACAAATGTCGTCATACGAACTTGAAGCAATCAGAGCCGGTGAATTTCAAGCTGG	2700
Db	2641	ATCGTTACAAATGTCGTCATACGAACTTGAAGCAATCAGAGCCGGTGAATTTCAAGCTGG	2700
Oy	2701	ACATGGCAAAACTGCTATGGGTGAGAGTGGGGCTTGACCGGGCTATTCAACGTTTGTGA	2760
Db	2701	ACATGGCAAAACTGCTATGGGTGAGAGTGGGGCTTGAGCGGGCTATTCAACGTTTGTGA	2760
Oy	2761	TCTGCGCGGATTTGAAGTCAATACATCGCGGTTACAGGCAAGAGCGAGTCACCGCAATC	2820
Db	2761	TCTGCGCGGATTTGAAGTCAATACATCGCGGTTACAGGCAAGAGCGAGTCACCGCAATC	2820
Oy	2821	TGCTGATCAACACTCAAGCTGCGCCAAATTTCTATTGACCTCTGCAACGATCAAGACT	2880
Db	2821	TGCTGATCAACACTCAAGCTGCGCCAAATTTCTATTGACCTCTGCAACGATCAACACT	2880
Oy	2881	TCAACACCTTCTCAGCGCCGGCCATTCACGATGAGAAATGCAATCTGTTTCTTGAACGG	2940
Db	2881	TCAACACCTTCTCAGCGCCGGCCATTCACGATGAGAAATGCAATCTGTTTCTTGAACGG	2940
Oy	2941	AGGACGACCTCCGCGCTTATCTCGTCAAGGCAAGGCTGAGACATGAGCGAGAAACGAGC	3000
Db	2941	AGGACGACCTCCGCGCTTATCTCGTCAAGGCAAGGCTGAGACATGAGCGAGAAACGAGC	3000
Oy	3001	ATGGGTTCTATCGGACTTCGTTGCAATAGCATGATCAAGTGGCGGAGATGATTCCA	3060
Db	3001	ATGGGTTCTATCGGACTTCGTTGCAATAGCATGATCAAGTGGCGGAGATGATTCCA	3060
Oy	3061	ATGTGGCTGACACTATGTGTGTCAAGCTCATTCGGCGCTACTGCACTTCAGTGGCGTCA	3120
Db	3061	ATGTGGCTGACACTATGTGTGTCAAGCTCATTCGGCGCTACTGCACTTCAGTGGCGTCA	3120
Oy	3121	ATGTTCTGATCAAGATCTGACCTCAATATCGCTTCTTGAACTTTCGTCGCTTATCT	3180
Db	3121	ATGTTCTGATCAAGATCTGACCTCAATATCGCTTCTTGAACTTTCGTCGCTTATCT	3180
Oy	3181	GCAATGCAAACTCTGAAAAGAGGGCAAAAGGCCAGATTTTGTGCAATGTCGCGCGCTG	3240
Db	3181	GCAATGCAAACTCTGAAAAGAGGGCAAAAGGCCAGATTTTGTGCAATGTCGCGCGCTG	3240
Oy	3241	CTTGCAATGATGATCGGGGCTCTACTGGCGCTTATTCGGGAGTCTCCGTGCCACCTCGAAG	3300
Db	3241	CTTGCAATGATGATCGGGGCTCTACTGGCGCTTATTCGGGAGTCTCCGTGCCACCTCGAAG	3300
Oy	3301	GTCGACCGGCTACCCCAACCAATGCTTTCATATGCACTGTCTGGGCTCCGGCCGTTTGTGG	3360
Db	3301	GTCGACCGGCTACCCCAACCAATGCTTTCATATGCACTGTCTGGGCTCCGGCCGTTTGTGG	3360
Oy	3361	CTGGATGGAATGCTTATCTGTGCGGAGGTTTTTTTCGCCGAGGAAAACGAAATTTGTGC	3420
Db	3361	CTGGATGGAATGCTTATCTGTGCGGAGGTTTTTTTCGCCGAGGAAAACGAAATTTGTGC	3420
Oy	3421	GAAAGCTCATACGAGATCGTCCCTGATCTATGACGAGAGTTAATCTGCTCTTGTTCGGGC	3480
Db	3421	GAAAGCTCATACGAGATCGTCCCTGATCTATGACGAGAGTTAATCTGCTCTTGTTCGGGC	3480
Oy	3481	TGTGCAATTTGCGTGGGACTCAAAATTCGATATTCGCTTCTCATATGGGGATATCTTG	3540
Db	3481	TGTGCAATTTGCGTGGGACTCAAAATTCGATATTCGCTTCTCATATGGGGATATCTTG	3540
Oy	3541	CTCTCTTCCAAACGCGCCTGAGTCAAGCAATCTCGCCGACGGAATGAGAGGTTCACTC	3600
Db	3541	CTCTCTTCCAAACGCGCCTGAGTCAAGCAATCTCGCCGACGGAATGAGAGGTTCACTC	3600
Oy	3601	GCCAGATTTGAAGATGTCCTTCTCATCTTGGAAGCTTGATCTGTGCGAATCGGGGAG	3660
Db	3601	GCCAGATTTGAAGATGTCCTTCTCATCTTGGAAGCTTGATCTGTGCGAATCGGGGAG	3660
Oy	3661	GCGTTTGTGGGTCTTTTATCAACATGTCGAAATGGGGTTTTCTTGCAATTAGTTGGGTGG	3720
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Query Match	100.0%	Score 7142	DB 24	Length 7142
Best Local Similarity	100.0%	Pred. No. 0		
Matches 7142	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	1	CGCGTAAGAAGACAGACAGAGTCCGTAAGACATTAAGAAAGCTTTTAGAGCAGCAACGA	60	
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Query	361	CGCCGAAGGTCACCAATTTCCGACGCGAGGTTTCTCGCTGCATTAATTTTCTTTC	420	
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QY	481	ATTGGGTATTGTGCAAAATTAATCTCATATGATTTGCAATTTTAAAAAGACAAGATAGGCTCA	540
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QY	541	CATTGTGACGAATATGACTGTGGCAAAACCCCAATCGCTAAATGAGTGTGTTCATGG	600
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QY	601	ATTAACAAGTTGCGAAAGATGTCGAAGTGAAGAAGGGCTCCATCAAGGCGACCTTCAAG	660
Db	601	ATTAACAAGTTGCGAAAGATGTCGAAGTGAAGAAGGGCTCCATCAAGGCGACCTTCAAG	660
QY	661	CTGCTGTTCTGAAGTCGAAGAAGAGGTGCAATCGGAGTGAAGCCCTCAAGGCTGCGTCG	720
Db	661	CTGCTGTTCTGAAGTCGAAGAAGAGGTGCAATCGGAGTGAAGCCCTCAAGGCTGCGTCG	720
QY	721	CTTAAGTAAACATCCGGCGGGTGGCGGCAAAAGCTACCCGCACTTAATAGCCCTCGCTTCA	780
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QY	781	CGGAGTGTTCGCAATGGAATTTCGTCMAAGATTGTAATCGAACCGCTCTTTCACCTCCG	840
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Db	961	GGTAGACGCTGTTGAGACGCTATCCGATTACGATCCGACGAAAGTGCGCGCAGCAATCGA	1020
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QY	1321	GTCCGTGCAATTCGGTCAATGGAAGAAGCACCGCTTCGGAACGAACTGTGCTGATTAAT	1380
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QY	1381	CACATTTGCTCTCAACTATATGCGGCGCGCAAAAGACGATACCGTCAACATGTATGCACTGG	1440
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QY	1441	CGAGCATCTGCGAAGAGCGCGTCCCATCTCGGAGAGAGCGGACACCCCATGGAATTTACGT	1500
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	Matches	93;	Conservative	0;	Mismatches	84;	Indels	0;	Gaps	0;
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Db	540	ATGACGGCTCCAGACAGACGCGCTGCGCATCCCGACCCCGAGCGAGCGGACCC								481
QY	6561	GCTGCTGCTTGAACGGCTATGCTGTCTCGAAGCAACGGCGCGCTTCGTGACAAGC								6620
Db	480	GGCGCGCGCATGCCCGCTGCGAGCGCGAGCAAGCGTGGCGCGACGGCGGCCAGC								421
QY	6621	TNATCAGTTGCGAGTTCAAGATGCGCGCGAGCGCGAAGAGCGCGCTGTCAAGC								6677
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 Job time : 16719 secs

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s) Nakamura, Y., Sato, S., Asamizu, E., Kato, T., Sasamoto, S.,

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Submission
1 (05-DEC-2000) Takahashi Kazuwa DNA Research

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QY	4966	TCATGAGAGCAAGCAAAACCCGATCTTGATTAACGCTCTCCGTGTTGATTGATTTCC	5025
Db	51106	YKTKCYGCAATKSMANAYTOSMRKQGTKSAMWYSMCSCKABAASGMVKCMKMGCGY	51165
QY	5026	GTCGGCGGTCAAGCCGGAATTCGATTGGGAAATTGCCAACAATCTAAGAGGTGCCGAAG	5085
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QY	5086	CATATTTTCAAGGCGTATGACCCCGTAAACATCTGGTTGCGATGTTTCTCGGATCGGT	5145
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QY	5146	ATCGAGATTAACCCGATGCTGAGGCGCGAAATTGAGCGAGATGCCAGAGAAATGATCGC	5205
Db	51285	SKMTYTTCTYKTYKTKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYK	51344
QY	5206	AGCAACCAAGTTTCCGTTCAACCCGATCTCACGCTGACCCG--CGCTATCGAGCCAAAGC	5264
Db	51345	WRGAKYMSMTSKTSGSRMTCMWSBWTCTCSMTSTCTCMGCTCTCSMSKGYTSRSC	51404
QY	5265	TGCAATCAGGCTCCAGTTCGCTCTCTTAAAAACGGCCGATCAAT--TTGATCTTGCTCT	5322
Db	51405	YAWMSKSYSTSYCMRCOMSYGMSKRSCTRBRKTYTMSWRKYKYCKMMSMAMGMYKGG	51464
QY	5323	CGCTTCGTGACCGCGGTTTTGGAAGTGTGAAGACGGGAAATTCACCGGTGACAGATCT	5382
Db	51465	SKWTTYYWYTGTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYK	51524
QY	5383	TCCATAAAAAACGATCTTCGGTTGAGACGGCGTCAACCGCATTTAGTGTTTCCCTGG	5442
Db	51525	SCATCAACCTISGMCCTCCCMRKRYKYSMTMCMCMGTYTSMNMTSMKSGMYR	51584
QY	5443	ATGACGGGCGCTATTATTAACACTGAGACAGATCGGTTGTTTTCCGACGCTATCGG	5502
Db	51585	SMSTMTKMSKYAATGKMYTYRMMWMMWMMKMTYYACKTYMCAAMYSMMSMRAT--RA	51643
QY	5503	GTAATCTACGGAGGGGTCAATGCAATATGATATTTGGCGCTGAGGTATACATGTGGCGT	5562
Db	51644	MTWGCAAGIRKMWGMATGMTTMTTAYCWCYTMAGSSCMACCTYYCASMGTGYSMAKST	51703
QY	5563	ATCAACCGCGCTCGTCTTGCCGATGCTACTCGAC--CTTGACACATATTAGGTACT	5621
Db	51704	KMMNCCTCCMSMMWCYCMSSYKTKTYTYSYRACMTSMCKSAVSCMYMSAACKSSYC	51763
QY	5622	CTATCGATGTGGCGTCCCTCTATGACAGCTCTATACAGACCGGCTTGCAAGACCGCT	5681
Db	51764	AKRSGCYKRYGMSWYTSGRSMWYTTSTYSCTMWSMMMSYMSWSKSCYTYSCKMRKC	51823
QY	5682	CCTGAGACCTGATCAATAGCGGTGACATCTCCAGGAAATAGCCGTTATGATTAATCA	5741
Db	51824	WCMSTMRSAACCTWRBMTSCYTWSRSTGMWSK--GWCCKCYRBSCCMSMTGYCKXG	51881
QY	5742	TAGCGCAGACGGGAATGCTGCGAACTGAAGAAGCGCAGACATCGTTTTCTCTGA	5801
Db	51882	KSMWKAATGKMSCARSMSCYCGKMRBRASCMGYCKMSMKTCMMBSYTTCTCYCG	51941
QY	5802	TGAACGCCGTGGCGCAGTCGTCGTTTTGGCGCTAAGCGCTGACCAGCGGGCGGAACA	5861
Db	51942	YCMWGGKTKWRSSYSKCYKKSMTKYSMRGMSYCSRSRYWYSRFRMRKCMGMWTRAS	52001
QY	5862	GCGACCGGTCTTTATGCGCGCTTGCAACAAGACGAGCGAGCGCTTGAGGTGCGAGAA	5921
Db	52002	KGKSYNSNSWGMWNGKTSYWCASAYAMSCKMRBSATSMGCCYMSYRBSACMSWSTDS	52061
QY	5922	TGCTTTCCGGGGGCGAAGCTGAAGAAGTAAACGCCGCTTGTTGTGTGCTACTAATGAA	5981
Db	52062	MESYSTSTRSCMSCKMRGMSYTSRMRGGCAGMSCYRKSCKRRGSMGMSWTKSKGT	52121

LOCUS	166494	166494	7218 bp	DNA	linear	PAT 28-DEC-1997
DEFINITION	Sequence 14 from patent US 5670367.					
ACCESSION	166494					
VERSION	166494.1	GI:2724471				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 7218)					
AUTHORS	Donner, F., Schefflinger, F. and Falkner, F. Gunter.					
TITLE	Recombinant fowlpox virus					
JOURNAL	Patent: US 5670367-A 14 23-SEP-1997;					
FEATURES	Location/Qualifiers					
source	1..7218					
	/organism="unknown"					
BASE COUNT	1944 a 1491 c 1486 g 1929 t	368 others				
ORIGIN						
Query Match	0.7%; Score 49.6; DB 6; Length 7218;					
Best Local Similarity	7.9%; Pred. No. 0.22;					
Matches	34; Conservative 211; Mismatches 185; Indels 0; Gaps 0;					
QY	3765	TTTTTCACTTGTGGGAATTGACGAGCGGACTTGCGATTGGGCTTGCAGCTCACTACCC	3822			
DB	996	TTTTTCTCTGTTGGCCATACGCTCACGAATTATTCGAGCTTGCTGCAGGCTGAGG	1055			
QY	3825	GAACTTTGATTAGCGCGCGCCGCTTCCCGCTGCACGCTTGATCGCGTTTACAGC	3884			
DB	1056	GAGCTTGCGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1115			
QY	3885	ACGATTTCGTGCTCTGCTTCTTGATCTACGTTGATTAATAGGTGAGCAATCGGAC	3944			
DB	1116	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1175			
QY	3945	ATATTGTCTCCCGCTGCTGCGGATGCGGATGCGGCTTTCCTGATCTGCGACGG	4006			
DB	1176	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1235			
QY	4005	CTGCACTTGTGTTGGGATATACGCTGCCAAAGCTGACGAGCACTCACGAT	4064			
DB	1236	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1295			
QY	4065	CTCAGCGCATGTACATCACTGACCTCTGAGATGATCTCGGCTGCGCGCGCTTGGGC	4124			
DB	1296	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1355			
QY	4125	TGCGTTCAAGCGTTGCGCATGCTTTGGTCTTTGGACGCGCTTCTTGCAATCTCCATT	4188			
DB	1356	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1415			
QY	4185	CCCGCGCTTC	4194			
DB	1416	TTTTTTTTTTTT	1425			
RESULT 10						
LOCUS	E32986	10732 bp	DNA	linear	PAT 18-JUN-2001	
DEFINITION	Gene encoding cellulose synthetizer.					
ACCESSION	E32986					
VERSION	E32986.1	GI:13022340				
KEYWORDS	JP 2000060568-A/1.					
SOURCE	Vigna angularis (adzuki bean)					
ORGANISM	Vigna angularis					
	Bukerjota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					

Db	208	YYCGSGYCGSSKKMKMKMSKSCMBRMTCSWMCSCVTCYYGAMCWSGCMSEMTMGSGCCTR	149
Oy	2910	GATGAGAAATATGCATCTGTTCTTTGAAGCGGAGACGACTCCGCTTTATCTGTCACG	2968
Db	148	GMKMSKSKSMCKCKKSCCTKCYSTGYRRYCKMKWYSYKCYCYCYWMSYMMKMC	89
Oy	2970	GCAGGCTAGACATGACGACGAAACACAGATGGCTCTATCGAGCTTCGTTGCAATAC	3029
Db	88	MCSSSCSSWMSCAVSTSTSTBRMSMTATAAKKCMCSSGATMRMSCKMTSKYSCKITG	29
Oy	3030	GCATCGATCAGTTGGCCGAGATGATTC	3057
Db	28	SKCTKRYKYYCYWSSGYSMCTSETYS	1
RESULT 6			
AX655393		2000 bp	linear
LOCUS	AX655393	DNA	PAT 22-MAR-2003
DEFINITION	Sequence 5263 from Patent WO03000898.		
ACCESSION	AX655393		
VERSION	AX655393.1		
KEYWORDS	GI:29158207		
SOURCE			
ORGANISM	Oryza sativa		
REFERENCE	Oryza sativa		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
TITLE	Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitlam, S., Xie, Z., Zhu, T. and Zou, G.		
JOURNAL	Plant genes involved in defense against pathogens		
FEATRES	Patent: WO 03000898-A 5263 03-JAN-2003; Syngenta Participations AG (CH)		
source	Location/Qualifiers		
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	/organism="Oryza sativa"		
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BASE COUNT	336 a 265 c 284 g 363 t	752 others	
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Query Match	0.8%; Score 56.6; DB 6; Length 2000;		
Best Local Similarity	9.6%; Pred. No. 0.002;		
Matches	73; Conservative 347; Mismatches 336; Indels 3; Gaps 2;		
Oy	623	CGAAGTGAAGAGGCGCTCCATCAAGCGACCTTCAAGCGCTGTTCTTGAAGTGAAGAC	682
Db	4	CSAGKSCSSCWSRGRRRMYGAMMSCAMGSSRMSRKMSKRYKSSCGKCKMTTRK	63
Oy	683	GAAGGTGCACATCGGAGGTAGCCGTCACAGGCGTGCCTTAAATGAACATCCGGCGGT	742
Db	64	SKWYSASSASGRTGSKMSGSGTSGKMKRYRKRMRGRGRMRMRMRMGVYRCA	123
Oy	743	GGCGGAAACGTACCCGCCACTATCCCTCGCTTCAACGGAGATTTTCGATGACTTC	802
Db	124	RSGRNAGSGRMWGKMSMYMMVYANGCS -CBKXSKSGSWKTCRRARGSGMS	182
Oy	803	GTCCACAGATTGTAATGACCGCTCTTTCCACTTCGCTACTACAGCTGACGCTTAT	862
Db	183	GAKYSGMSRKMMSGCRSGCGRRASYSRYGTSRKTYGKTKTYTSASRCMAVMT	242
Oy	863	CTATTCGGGAGTTCGACAGGTGCGCTCGGAGCGAGACATCACTCAACATGCGCTATT	922
Db	243	SYSNACSSYTCRSKRSMKMMKMKRMSRYGMSYKMMCTAYIKSYSWCTMY	302
Oy	923	TGGACATT--TGTCGACATTCAATGACAGCCGAGAGTCTGTGTAGACGCTTTGACGC	980
Db	303	RGGGWRGATRYWGRGYSMAVYKMYRYGKMKRGMWAGRMMSRMSKWSKACYM	362
Oy	981	TATCCGATTACATCCGACGAAGTGGCCGACGACATGGAAGGACATGCGAGTGGGCA	1044
Db	363	RRMRMRTRRRWAKSSSTSRKRRKCMRRTKRYKRMGYSRMSCKRRMRKCRSGR	422

Oy	1041	TCATCGAAGCGGTGGCGTTGAAAGACCGCAATTGATTCCTTTGACGGTGAAGCGTCAC	110
Oy	1101	ATGTCGACAGGCGATGGAATATTCACCTGTCTCAATGCGATCGATCGATCAATTATC	1160
Oy	423	AWKMGCGCMTCRMKKSIGMMFMWSMKMASRYKMMSMYMRKKKCSRTTWMGTRGMM	482
Oy	1161	TGATGTGGAAGAGCGTTAAACGCCAGACCTTTGAACAAATGACAGCAATTTGTGAGG	1220
Oy	543	WYRKGYWAGMMWKKRYKMRYMMYMMMYRKYKSKCSWYKCMYSYASCMKSFARAKMC	602
Oy	1221	AGCGTGTTCCTCGCAATTTTCACAGAGCCGCCAATCTCGACCGAATATGATTTGCCA	1280
Oy	603	KRSMWSAMSKMSRSCRCRKAASRSSAKRYAMMGMTGSRMSRMSYTCYMRKMSMK	662
Oy	1281	GTTTAGGCGCGCTACAGCGTTTCGAATTAATACTGGCGTCCGTCGATTCGTCATG	1340
Oy	663	STCTWMTYMSKTYTAXKGSYWRYYRYRAMCMYMMWYRRYRYSYVTYMAWYTSIRMA	722
Oy	1341	AGAAGGACCGCGCTTCGAGACGAACTGTCGCTCATATPA	1379
Oy	723	MKYSGRYWTSMYKCKCSMKYRSWMYMMWMAKTWMM	761
Db			
RESULT 7			
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LOCUS	AF429315	125020 bp	DNA linear PRI 18-JAN-2002
DEFINITION	Homo sapiens junctophilin 3 (JPH3) gene, partial cds.		
ACCESSION	AF429315		
VERSION	AF429315.1	GI:17646244	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 125020) Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingeroll,Ashworth,R.G., Plesher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.		
TITLE	A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2		
JOURNAL	Nat. Genet. 29 (4), 377-378 (2001)		
MEDLINE	2 (bases 1 to 125020)		
PUBMED	21583737		
REFERENCE	11694876		
AUTHORS	Holmes,S.E., Ingeroll,Ashworth,R.G., Ross,C.A. and Margolis,R.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA		
FEATURES	Location/Qualifiers		
source	1..125020		
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	/note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)"		
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	/gene="JPH3"		
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	/gene="JPH3"		
	/product="junctophilin 3"		
	complement(<36507..36887)		
	/gene="JPH3"		
cds	/note="component of the junctional complex between plasma membrane and endoplasmic reticulum"		
	/codon_start=1		

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Gene name confidence : hypothetical"
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/translation="MSVLSILITFLVIVLVVNLPLDRTKQIVIVIIIGLL
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complement(746..1804)
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 QY 5821 GTCCGTTTGGGCGGTAGGCGTGAACCGAGGCGGCGAAGCGGACCGGTCTTATAGG 5880
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 Finan, T.M., Weidner, S., Wong, K., Buhrester, J., Chain, P.,
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 Submitted (07-JUN-2001) Weidner S., Universitaet Bielefeld,
 Biologie IV (Genetik) Universitaetstr 25, D-33615 Bielefeld,
 Germany
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 Submitted on behalf of Universitaet Bielefeld, Biologie IV
 (Genetik) Universitaetstr 25, D-33615 Bielefeld, Germany and
 Department of Biology, McMaster University, 1280 Main Street West,
 Hamilton, Ontario, L8S 4K1 Canada
 mailto:Stefan.Weidner@genetik.uni-bielefeld.de
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REFERENCE
1 Triplett, E.W. and Herlache, T.C.
Biological control of crown gall disease
Patent: WO 0213614-A 7 21-FEB-2002;
JOURNAL WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
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Db 6181 GACATTAATGTTATGAGGAGTGAATTTGTACCCAGGCGCTTCGATGAGCGCGGAGCTT 6240
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Oy 6421 GATAGATTCGAGAGTGTGCGGCTGTCAGGCGGATTCGATTCGATTCGCGGCTGTTG 6480
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Db 6541 CATGAGAGGCGATCAAGTTCGCTGCTTCGACGCGCTATGCTGCTCTCGGAAAGCAAG 6600
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QY	2821	TGCTGATCAACACCTCACAGCTCGCCCAATTTCTATTGTGACCTCTGCAACGATCAACGACT	2880
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QY	2881	TCACACCTTTCTCAAGCGCCGCGCATTCACCATGTGAAAAATGCAATCTGTTTCTTGAACGG	2940
Db	2881	TCACACCTTTCTCAAGCGCCGCGCATTCACCATGTGAAAAATGCAATCTGTTTCTTGAACGG	2940
QY	2941	AGGACGACCTCCCGCTTATCTCGTCAACGCGAGGCTAGAGCATAGGACGCAAAAACGAGC	3000
Db	2941	AGGACGACCTCCCGCTTATCTCGTCAACGCGAGGCTAGAGCATAGGACGCAAAAACGAGC	3000
QY	3001	ATGGGTTCTATCGAATCTGTTGCAATATCGATCGATCATGTTGGCGGAGAAATGATTCCA	3060
Db	3001	ATGGGTTCTATCGAATCTGTTGCAATATCGATCGATCATGTTGGCGGAGAAATGATTCCA	3060
QY	3061	ATGAGCGTCGACATATGCTGCTACGCGCTACGCGGCGTACAGCACTTCAGGTGCGTCA	3120
Db	3061	ATGAGCGTCGACATATGCTGCTACGCGCTACGCGGCGTACAGCACTTCAGGTGCGTCA	3120
QY	3121	ATGTTTCTGATCAACATCTGACCCCTCATATCGCTTTTCTGAACTTTTGTCTGCTTATCT	3180
Db	3121	ATGTTTCTGATCAACATCTGACCCCTCATATCGCTTTTCTGAACTTTTGTCTGCTTATCT	3180
QY	3181	GCATGCAACATCTGAAAAGAGGGGCAAAAGGCCGACATTTGCTGCAATGCTCGCGCTG	3240
Db	3181	GCATGCAACATCTGAAAAGAGGGGCAAAAGGCCGACATTTGCTGCAATGCTCGCGCTG	3240
QY	3241	CTTGCAATGATATCGAGGGTCTACCTGCGGCTTATACGCGATCTCGGTGCGCAACCTCGAAG	3300
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QY	3301	GTGCAACCGGTAACCCAAACCAATTGCTTATAGACATGCTCTGCGCTCGGCGGTTTGTGG	3360
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Db	3421	GAAAGGTCATACAGGATCGTGCCTGATCTATGACGAGATTAACTGCTCTTTGTCGGGC	3480
QY	3481	TGTGCAATTTGCTGCGACTGAAATTTGATCATATGCTTCTCATCGGCGTATATCTTG	3540
Db	3481	TGTGCAATTTGCTGCGACTGAAATTTGATCATATGCTTCTCATCGGCGTATATCTTG	3540
QY	3541	CTCTTTTCCAAACGCGCCTGGCGCTACGCGCAGATCTTGCAGACGGAATGAGGTTCACTC	3600
Db	3541	CTCTTTTCCAAACGCGCCTGGCGCTACGCGCAGATCTTGCAGACGGAATGAGGTTCACTC	3600
QY	3601	GCCAGGATTTGAAGGATGTTTCTTCACTTCGGAAGCTTGATCTGTGCGAAATCGGGCAG	3660
Db	3601	GCCAGGATTTGAAGGATGTTTCTTCACTTCGGAAGCTTGATCTGTGCGAAATCGGGCAG	3660
QY	3661	GGCTTTTCTGCGCTTTTATCAACATGCTCGAAATGCGGATTTCTTGCAATTAATTTGAGTGG	3720
Db	3661	GGCTTTTCTGCGCTTTTATCAACATGCTCGAAATGCGGATTTCTTGCAATTAATTTGAGTGG	3720
QY	3721	TGTTGGCAGCAAAAGTTTCCGCAATTCGCGGTTTTTATTTCCGTTTTCACTTTGAGTGG	3780
Db	3721	TGTTGGCAGCAAAAGTTTCCGCAATTCGCGGTTTTTATTTCCGTTTTCACTTTGAGTGG	3780
QY	3781	AATTGACGAGCGGACTTGGCATTTGGGCTTGAACCTCAGTCAACGGAACGTTGATTATACG	3840
Db	3781	AATTGACGAGCGGACTTGGCATTTGGGCTTGAACCTCAGTCAACGGAACGTTGATTATACG	3840

QY	3841	CGGCGCCGTTTCCCGGGCTGCACGCTTGAATCGCGCTTAAACGACGATATCGTTGGCT	3900
Db	3841	CGGCGCCGTTTCCCGGGCTGCACGCTTGAATCGCGCTTAAACGACGATATTCGTGGCTCT	3900
QY	3901	GCTTCTTGATCTACGTTGGATTAAATGGTGTGAGCAATCGGACATATTTGCTCTCCGC	3960
Db	3901	GCTTCTTGATCTACGTTGGATTAAATGGTGTGAGCAATCGGACATATTTGCTCTCCGC	3960
QY	3961	TGTGCGTTGCGGAGTTGGGCTACTTTTCTTGATCTGCGACGGGCTGACGTTGTGGTT	4020
Db	3961	TGTGCGTTGCGGAGTTGGGCTACTTTTCTTGATCTGCGACGGGCTGACGTTGTGGTT	4020
QY	4021	GGGGATATACGCTCCGCAAGCTGACGGAGGAGACTACGCATCTCAAGGCGCAFTTCAT	4080
Db	4021	GGGGATATACGCTCCGCAAGCTGACGGAGGAGACTACGCATCTCAAGGCGCAFTTCAT	4080
QY	4081	ACCTAGCCCTTGAGAGTACTCTCGGCGTGGCGGCGCTTGGGCTCGGTTCAACGTTGG	4140
Db	4081	ACCTAGCCCTTGAGAGTACTCTCGGCGTGGCGGCGCTTGGGCTCGGTTCAACGTTGG	4140
QY	4141	CCATCGCTTGGTCTTGGGACCGCTGTCTTGCAATCTCCATCTCCGCGCTTCAAAATC	4200
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QY	4441	GAAGCTACCAATGCCCTTCAACAGAGAAATCCGTCACCCGCGGTTGAGCTTGTGGTAAACG	4500
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Db	4501	CGGCAACATCTGTGCTGAGTGGCGGCAACAATCTCCAGAGATTTGCCCATCTCCCGG	4560
QY	4561	CGCAAGGACAGAAATTGAACAACGCGGCTCAATGAGTGTTTAGAGCGCGGCTGGAACGCTCGG	4620
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QY	4621	TTTTGCAGAAATACGAGAGTCTCTTCTTAAGTTGGCGACGATCCGACGAGAGCGTTTCAACA	4680
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QY	4741	GCGGAGCATGTGCGTTGGGGTTCGCAATTCGCAAGACGACCGAAGCGGACGTGAGACT	4800
Db	4741	GCGGAGCATGTGCGTTGGGGTTCGCAATTCGCAAGACGACCGAAGCGGACGTGAGACT	4800
QY	4801	GCAACTGATGAACCCATGCGATGAGATGGGTGCGGAGAGATTAAGGTCGCGCGGAACCC	4860
Db	4801	GCAACTGATGAACCCATGCGATGAGATGGGTGCGGAGAGATTAAGGTCGCGCGGAACCC	4860
QY	4861	GGCGTGTGCGAGGCTTCCCTTCGCAACGACCAAAATCGCTTGTGGAAGGACGCGGTG	4920
Db	4861	GGCGTGTGCGAGGCTTCCCTTCGCAACGACCAAAATCGCTTGTGGAAGGACGCGGTG	4920
QY	4921	CGATCGATGATGCTCACTCAATTAAGTGAATACAGCGCGGTGAATTATTCATGAGACAAACA	4980

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VERSION AX385012.1 GI:19578140
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ORGANISM Rhizobium leguminosarum bv. trifolii
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
REFERENCE 1
AUTHORS Triplett, E.W. and Herlache, T.C.
TITLE Biological control of crown gall disease
JOURNAL Patent: WO 0213614-A 1 21-FEB-2002;
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TITLE DNA sequence and mutational analysis of genes involved in the production and resistance of the antibiotic peptide trifoliotoxin

JOURNAL J. Bacteriol. 175 (12) , 3693-3702 (1993)

MEDLINE 93285981

PUBMED 8509324

COMMENT Original

FEATURES

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Matches 7142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 GTTTCCTGCGGCTCTTGTCTCCACACCACTCATATTTCGGCAGAAATTCGGTATGCTC 300

SUMMARIES

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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(without alignments)

17490.365 Million cell updates/sec

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Scoring table: IDENTITY_NUC
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Gapext 1.0

Searched: 2888711 bsgs, 20454813386 residues

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Post-processing: Minimum Match 0%
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36:	em	htg	mam:
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Pred. No. is the number of results predicted by chance to have a

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	Rhizobium leguminosarum			
	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
	Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.			
REFERENCE	1 (bases 1 to 7142)			
AUTHORS	Breil,B.T., Ludden,P.W. and Triplett,E.W.			

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TITLE DNA sequence and mutational analysis of genes involved in the production and resistance of the antibiotic peptide trifolioxin
JOURNAL U. Bacteriol. 175 (12), 3693-3702 (1993)
MEDLINE 93285981
COMMENT PUBMED 8509324
FEATURES Original Source
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Location/Qualifiers

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OY	601	ATTAACAAGTTGCGAAGATGTCGAATGGAAGAGGCTCCATCAAGCGACCTTCAAG	660
Db	601	ATTAACAAGTTGCGAAGATGTCGAATGGAAGAGGCTCCATCAAGCGACCTTCAAG	660
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OY	1201	GGACAAGCAATTTGTGAGAGAGGCTGTTCCGTGCAATTTTCAAGAGCGGCAACTCTCG	1260
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OY	1261	ACCGAATATGATTTGCCAAGTTTGTAGTCCGCTGACAGCGTTGCAATTCATTAATCTCGC	1320
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OY	1321	GTCCGTGCAATTCGGTCAATGGAAGGCAACCGCTTCCGAACGATGTGCTCGATTAAT	1380
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Db	1501	GCTTGTCCGCGATGAGATATGCAAGGTATCGAAGCTGAGCGTATATCACTACATATGTCGCCA	1560
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LOCUS Sequence 1 from Patent WO0213614.
ACCESSION AX385012
VERSION AX385012.1 GI:19578140

SOURCE Rhizobium leguminosarum bv. trifolii
ORGANISM Rhizobium leguminosarum bv. trifolii
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.

REFERENCE 1
AUTHORS Triplett, E.W. and Herjache, T.C.
TITLE Biological control of crown gall disease
JOURNAL Patent: WO 0213614-A 1 21-FEB-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION (US)

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